

Appendix A1

Applications copy

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 25, 2004, 05:24:29 ; Search time 71 Seconds
(without alignments)
1229.090 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPAPSPQRILGILLIL.....GDASTGMSVSRILIEELPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
3: /cn2_6/ptodata/1/pubppa/US05_PUBCOMB.pep.*
4: /cn2_6/ptodata/1/pubppa/US04_PUBCOMB.pep.*
5: /cn2_6/ptodata/1/pubppa/US03_PUBCOMB.pep.*
6: /cn2_6/ptodata/1/pubppa/US02_PUBCOMB.pep.*
7: /cn2_6/ptodata/1/pubppa/US01_PUBCOMB.pep.*
8: /cn2_6/ptodata/1/pubppa/US00_PUBCOMB.pep.*
9: /cn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
11: /cn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
12: /cn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
13: /cn2_6/ptodata/1/pubppa/US05_PUBCOMB.pep.*
14: /cn2_6/ptodata/1/pubppa/US04_PUBCOMB.pep.*
15: /cn2_6/ptodata/1/pubppa/US03_PUBCOMB.pep.*
16: /cn2_6/ptodata/1/pubppa/US02_PUBCOMB.pep.*
17: /cn2_6/ptodata/1/pubppa/US01_PUBCOMB.pep.*
18: /cn2_6/ptodata/1/pubppa/US00_PUBCOMB.pep.*
19: /cn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
20: /cn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1301 | 100.0 | 243 | 9 | US-09-834-759-514 |
| 2 | 1301 | 100.0 | 243 | 9 | US-09-938-418-7 |
| 3 | 1301 | 100.0 | 243 | 10 | US-09-946-374-352 |
| 4 | 1301 | 100.0 | 243 | 10 | US-09-946-374-431 |
| 5 | 1301 | 100.0 | 243 | 13 | US-10-006-867-122 |
| 6 | 1301 | 100.0 | 243 | 13 | US-10-052-586-366 |
| 7 | 1301 | 100.0 | 243 | 13 | US-10-007-805-514 |
| 8 | 1301 | 100.0 | 243 | 13 | US-10-063-547-122 |
| 9 | 1301 | 100.0 | 243 | 13 | US-10-063-551-122 |
| 10 | 1301 | 100.0 | 243 | 14 | US-10-174-590-366 |
| 11 | 1301 | 100.0 | 243 | 14 | US-10-176-758-366 |
| 12 | 1301 | 100.0 | 243 | 14 | US-10-175-737-366 |
| 13 | 1301 | 100.0 | 243 | 14 | US-10-063-616-122 |

| | | | | | | |
|----|------|-------|-----|----|-------------------|-------------------|
| 14 | 1301 | 100.0 | 243 | 14 | US-10-174-581-366 | Sequence 366, App |
| 15 | 1301 | 100.0 | 243 | 14 | US-10-176-483-366 | Sequence 366, App |
| 16 | 1301 | 100.0 | 243 | 14 | US-10-176-749-366 | Sequence 366, App |
| 17 | 1301 | 100.0 | 243 | 14 | US-10-176-914-366 | Sequence 366, App |
| 18 | 1301 | 100.0 | 243 | 14 | US-10-176-915-366 | Sequence 366, App |
| 19 | 1301 | 100.0 | 243 | 14 | US-10-063-569-122 | Sequence 122, App |
| 20 | 1301 | 100.0 | 243 | 14 | US-10-063-513-122 | Sequence 122, App |
| 21 | 1301 | 100.0 | 243 | 14 | US-10-063-513-122 | Sequence 122, App |
| 22 | 1301 | 100.0 | 243 | 14 | US-10-063-512-122 | Sequence 122, App |
| 23 | 1301 | 100.0 | 243 | 14 | US-10-173-706-366 | Sequence 366, App |
| 24 | 1301 | 100.0 | 243 | 14 | US-10-173-728-366 | Sequence 366, App |
| 25 | 1301 | 100.0 | 243 | 14 | US-10-175-752-366 | Sequence 366, App |
| 26 | 1301 | 100.0 | 243 | 14 | US-10-176-482-366 | Sequence 366, App |
| 27 | 1301 | 100.0 | 243 | 14 | US-10-176-757-366 | Sequence 366, App |
| 28 | 1301 | 100.0 | 243 | 14 | US-10-176-913-366 | Sequence 366, App |
| 29 | 1301 | 100.0 | 243 | 14 | US-10-180-552-366 | Sequence 366, App |
| 30 | 1301 | 100.0 | 243 | 14 | US-10-180-557-366 | Sequence 366, App |
| 31 | 1301 | 100.0 | 243 | 14 | US-10-076-622-514 | Sequence 514, App |
| 32 | 1301 | 100.0 | 243 | 14 | US-10-063-502-122 | Sequence 122, App |
| 33 | 1301 | 100.0 | 243 | 14 | US-10-173-700-366 | Sequence 366, App |
| 34 | 1301 | 100.0 | 243 | 14 | US-10-173-572-366 | Sequence 366, App |
| 35 | 1301 | 100.0 | 243 | 14 | US-10-174-579-366 | Sequence 366, App |
| 36 | 1301 | 100.0 | 243 | 14 | US-10-174-582-366 | Sequence 366, App |
| 37 | 1301 | 100.0 | 243 | 14 | US-10-174-588-366 | Sequence 366, App |
| 38 | 1301 | 100.0 | 243 | 14 | US-10-175-739-366 | Sequence 366, App |
| 39 | 1301 | 100.0 | 243 | 14 | US-10-175-740-366 | Sequence 366, App |
| 40 | 1301 | 100.0 | 243 | 14 | US-10-175-743-366 | Sequence 366, App |
| 41 | 1301 | 100.0 | 243 | 14 | US-10-175-748-366 | Sequence 366, App |
| 42 | 1301 | 100.0 | 243 | 14 | US-10-176-482-366 | Sequence 366, App |
| 43 | 1301 | 100.0 | 243 | 14 | US-10-176-747-366 | Sequence 366, App |
| 44 | 1301 | 100.0 | 243 | 14 | US-10-176-750-366 | Sequence 366, App |
| 45 | 1301 | 100.0 | 243 | 14 | US-10-176-985-366 | Sequence 366, App |

ALIGNMENTS

RESULT 1
US-09-834-759-514
Sequence 514, Application US/09834759
Publication No. US2002008598A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 514
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-759-514

Query Match 100.0%; Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPGPAPSPQRILGILLILQLPAPSSASIPKQKQAKLROREVVLDLYNMCICQGA 60
DB 1 MRPGPAPSPQRILGILLILQLPAPSSASIPKQKQAKLROREVVLDLYNMCICQGA 60
QY 61 GVPGRDGSFGANVITPTPGIPGRDGFKGKGCLEBSFESWTPTNYKQCSMSLNYGIDL 120
DB 61 GVPGRDGSFGANVITPTPGIPGRDGFKGKGCLEBSFESWTPTNYKQCSMSLNYGIDL 120

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QY 121 GKIARCTFKRMSNSALRVLPFGSLRLKCRNACCCORWYTFNGACSGPLPEIAIYYDQ 180
DB 121 GKIARCTFKRMSNSALRVLPFGSLRLKCRNACCCORWYTFNGACSGPLPEIAIYYDQ 180
QY 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 2
US-09-938-418-7
Sequence 7, Application US/09938418
GENERAL INFORMATION:
APPLICANT: Aebkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin L.
APPLICANT: Polakis, Paul
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wu, Thomas D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5009R1
CURRENT APPLICATION NUMBER: US/09/938,418
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/081,071
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 60/085,697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/097,022
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/101,922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/103,679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-09-938-418-7

Query Match 100.0%; Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGAPASPORAGLILLLILLOLPAPSSASEIRKQKQKQRLRRREVVDLYNMCLOSPA 60
DB 1 MRPGAPASPORAGLILLLILLOLPAPSSASEIRKQKQKQRLRRREVVDLYNMCLOSPA 60
QY 61 GVPGRDPSPGANVLPPTGPIGRDGFKEGKECELRSEFEESWTNNYQCSWSLNYGIDL 120
DB 61 GVPGRDPSPGANVLPPTGPIGRDGFKEGKECELRSEFEESWTNNYQCSWSLNYGIDL 120
QY 121 GKIARCTFKRMSNSALRVLPFGSLRLKCRNACCCORWYTFNGACSGPLPEIAIYYDQ 180
DB 121 GKIARCTFKRMSNSALRVLPFGSLRLKCRNACCCORWYTFNGACSGPLPEIAIYYDQ 180
QY 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 3
US-09-946-374-352
Sequence 352, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830FIC1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01

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GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: December 25, 2004, 05:24:29 ; Search time 71 Seconds
(without alignments)
1229.090 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPASPQRRLGILLULL.....GDASTGWNVSRIIEELPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1301 | 100.0 | 243 | 9 | US-09-834-759-514 |
| 2 | 1301 | 100.0 | 243 | 9 | US-09-938-418-7 |
| 3 | 1301 | 100.0 | 243 | 10 | US-09-946-374-352 |
| 4 | 1301 | 100.0 | 243 | 10 | US-09-946-374-431 |
| 5 | 1301 | 100.0 | 243 | 13 | US-10-006-867-122 |
| 6 | 1301 | 100.0 | 243 | 13 | US-10-052-586-366 |
| 7 | 1301 | 100.0 | 243 | 13 | US-10-007-805-514 |
| 8 | 1301 | 100.0 | 243 | 13 | US-10-063-547-122 |
| 9 | 1301 | 100.0 | 243 | 13 | US-10-063-551-122 |
| 10 | 1301 | 100.0 | 243 | 14 | US-10-174-590-366 |
| 11 | 1301 | 100.0 | 243 | 14 | US-10-176-590-366 |
| 12 | 1301 | 100.0 | 243 | 14 | US-10-175-737-366 |
| 13 | 1301 | 100.0 | 243 | 14 | US-10-063-616-122 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 14 | 1301 | 100.0 | 243 | 14 | US-10-174-581-366 |
| 15 | 1301 | 100.0 | 243 | 14 | US-10-176-483-366 |
| 16 | 1301 | 100.0 | 243 | 14 | US-10-176-749-366 |
| 17 | 1301 | 100.0 | 243 | 14 | US-10-176-914-366 |
| 18 | 1301 | 100.0 | 243 | 14 | US-10-176-915-366 |
| 19 | 1301 | 100.0 | 243 | 14 | US-10-063-569-122 |
| 20 | 1301 | 100.0 | 243 | 14 | US-10-063-513-122 |
| 21 | 1301 | 100.0 | 243 | 14 | US-10-063-515-122 |
| 22 | 1301 | 100.0 | 243 | 14 | US-10-063-512-122 |
| 23 | 1301 | 100.0 | 243 | 14 | US-10-173-768-366 |
| 24 | 1301 | 100.0 | 243 | 14 | US-10-175-728-366 |
| 25 | 1301 | 100.0 | 243 | 14 | US-10-175-752-366 |
| 26 | 1301 | 100.0 | 243 | 14 | US-10-176-482-366 |
| 27 | 1301 | 100.0 | 243 | 14 | US-10-176-757-366 |
| 28 | 1301 | 100.0 | 243 | 14 | US-10-176-913-366 |
| 29 | 1301 | 100.0 | 243 | 14 | US-10-180-552-366 |
| 30 | 1301 | 100.0 | 243 | 14 | US-10-180-557-366 |
| 31 | 1301 | 100.0 | 243 | 14 | US-10-076-622-514 |
| 32 | 1301 | 100.0 | 243 | 14 | US-10-063-502-122 |
| 33 | 1301 | 100.0 | 243 | 14 | US-10-173-700-366 |
| 34 | 1301 | 100.0 | 243 | 14 | US-10-174-743-366 |
| 35 | 1301 | 100.0 | 243 | 14 | US-10-174-579-366 |
| 36 | 1301 | 100.0 | 243 | 14 | US-10-174-582-366 |
| 37 | 1301 | 100.0 | 243 | 14 | US-10-174-588-366 |
| 38 | 1301 | 100.0 | 243 | 14 | US-10-175-739-366 |
| 39 | 1301 | 100.0 | 243 | 14 | US-10-175-740-366 |
| 40 | 1301 | 100.0 | 243 | 14 | US-10-175-743-366 |
| 41 | 1301 | 100.0 | 243 | 14 | US-10-176-488-366 |
| 42 | 1301 | 100.0 | 243 | 14 | US-10-176-492-366 |
| 43 | 1301 | 100.0 | 243 | 14 | US-10-176-747-366 |
| 44 | 1301 | 100.0 | 243 | 14 | US-10-176-750-366 |
| 45 | 1301 | 100.0 | 243 | 14 | US-10-176-985-366 |

ALIGNMENTS

RESULT 1

US-09-834-759-514

Sequence 514, Application US/09834759

Publication No. US2002008598A1

GENERAL INFORMATION:

APPLICANT: Jilang, Yulin

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jianshun

APPLICANT: Harlocker, Susan L.

APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.470C9

CURRENT APPLICATION NUMBER: US/09/834,759

CURRENT FILING DATE: 2001-04-13

NUMBER OF SEQ ID NOS: 547

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 514

LENGTH: 243

TYPE: PRT

ORGANISM: Homo sapiens

US-09-834-759-514

Query Match 100.0%; Score 1301; DB 9; Length 243;

Best Local Similarity 100.0%; Pred. No. 3e-118;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| QY | DB | QY | DB |
|----|--|----|--|
| 1 | MRPGPASPQRRLGILLULL.....GDASTGWNVSRIIEELPK 60 | 1 | MRPGPASPQRRLGILLULL.....GDASTGWNVSRIIEELPK 60 |
| 61 | GVPRGDSFGANVIRPGRDGEKGECLRESFESWTPTNYKQCSWSLNYGIDL 120 | 61 | GVPRGDSFGANVIRPGRDGEKGECLRESFESWTPTNYKQCSWSLNYGIDL 120 |
| 61 | GVPRGDSFGANVIRPGRDGEKGECLRESFESWTPTNYKQCSWSLNYGIDL 120 | 61 | GVPRGDSFGANVIRPGRDGEKGECLRESFESWTPTNYKQCSWSLNYGIDL 120 |

QY 121 GKIACCTFKMRSNSALRVLFSSGLRLKCRNACCCORWYFTFNGAECGGLPIEAIITYLDQ 180
DB 121 GKIACCTFKMRSNSALRVLFSSGLRLKCRNACCCORWYFTFNGAECGGLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 2

US-09-938-418-7
Sequence 7, Application US/09938418
Patent No. US20020161199A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin L.
APPLICANT: Polakis, Paul
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: P5009R1
CURRENT APPLICATION NUMBER: US/09/938,418
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/081,071
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 60/085,697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/097,022
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/101,922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/103,679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapien
US-09-938-418-7

Query Match 100.0%; Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPPRLRLGLLLLLLOLPAPSSASEIPIKQKQKQLOREYVDLYNMCIOGPA 60
DB 1 MRPOGPASPPRLRLGLLLLLLOLPAPSSASEIPIKQKQKQLOREYVDLYNMCIOGPA 60
QY 61 GVPGRDGSFGANVITGPTGIPGRDGFKEGKECECLRESFESWTPTNYKQCSMSLNYGIDL 120
DB 61 GVPGRDGSFGANVITGPTGIPGRDGFKEGKECECLRESFESWTPTNYKQCSMSLNYGIDL 120
QY 121 GKIACCTFKMRSNSALRVLFSSGLRLKCRNACCCORWYFTFNGAECGGLPIEAIITYLDQ 180
DB 121 GKIACCTFKMRSNSALRVLFSSGLRLKCRNACCCORWYFTFNGAECGGLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 3

US-09-946-374-352
Sequence 352, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Boctstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PICI
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01

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 PRIOR FILING DATE: 1998-10-26
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1301; DB 10; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 181 GSEPMNSTIHTSTSYEGLCEGIGAGLVVAIIVWGTCSDYPKGDASTGNVSRIIIE 240
 Db 181 GSEPMNSTIHTSTSYEGLCEGIGAGLVVAIIVWGTCSDYPKGDASTGNVSRIIIE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 4

US-09-946-374-431
 Sequence 431, Application US/09946374
 Publication No. US20030073129A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Batton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Christopher J.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Paoletti, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2830P1C1
 CURRENT APPLICATION NUMBER: US/09/946,374

CURRENT FILING DATE: 2001-09-04
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PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1301; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MBPQGPASPORLRLGLLLLLLLQLPAPSSASRIPKQKQALROREVDLYNGMCLQCPA 60
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DB 121 GKIAECTFTKMSNSALRYLFGSLRLKCRNACCCORWYFTFNGACSGCLPTEAIIYLDQ 180
QY 181 GSPENNSTINIRTSVSEGLCEGIGAGLVDAIWTGTSDDYKGSASTGMSVSRITIE 240
DB 181 GSPENNSTINIRTSVSEGLCEGIGAGLVDAIWTGTSDDYKGSASTGMSVSRITIE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 5
US-10-066-867-122
Sequence 122, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guirney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P323ORIC1
CURRENT APPLICATION NUMBER: US/10/006,867
PRIOR APPLICATION NUMBER: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29

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 72 PRIOR APPLICATION NUMBER: 60/119285
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APPLICANT: Smith,Victoria
APPLICANT: Matanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
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 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088722
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088740
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088811
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088825
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088863
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089090
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1301; DB 13; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGLLLLLLPAPESASEIRKQKQKOLQREYVLDLYNCKLOGPA 60
 DB 1 MRPGPASPORLRLGLLLLLLPAPESASEIRKQKQKOLQREYVLDLYNCKLOGPA 60
 QY 61 GVGGRDGGPGANVIRGTGIGRDPFGKGEKCELRSEFESWTPNYKQCSWSLNYGIDL 120
 DB 61 GVGGRDGGPGANVIRGTGIGRDPFGKGEKCELRSEFESWTPNYKQCSWSLNYGIDL 120
 QY 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCOMWYTFNCAEESGGLPTEAIITYDQ 180
 DB 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCOMWYTFNCAEESGGLPTEAIITYDQ 180
 QY 191 GSPENNSTINIRHRSVVEGICEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRITIEE 240
 DB 191 GSPENNSTINIRHRSVVEGICEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 7
 US-10-007-805-514
 Sequence 514, Application US/10007805


```
Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margareta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 514
; LENGTH: 243
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-007-805-514

Query Match      100.0%; Score 1301; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
QY 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
QY 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWTGSDYPKGDASTGMNSVSRILIEE 240
DB 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWTGSDYPKGDASTGMNSVSRILIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 8
US-10-063-547-122
; Sequence 122, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
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LENGTH: 243
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-063-547-122

Query Match      100.0%; Score 1301; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
QY 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
QY 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWTGSDYPKGDASTGMNSVSRILIEE 240
DB 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWTGSDYPKGDASTGMNSVSRILIEE 240
QY 241 LPK 243
DB 241 LPK 243
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```
RESULT 9
US-10-063-551-122
; Sequence 122, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
; LENGTH: 243
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-063-551-122

Query Match      100.0%; Score 1301; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASIEIPKQKQAOUREVVDLYNGMCLQGPA 60
QY 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPGRDSPGANVITGTPGIPGRDGFKEGKECLRESFEESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
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QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 10
 US-10-174-590-366
 Sequence 366, Application US/10174590
 Publication No. US20030008352A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jlan
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C42
 CURRENT APPLICATION NUMBER: US/10/174,590
 PRIOR FILING DATE: 2002-06-18
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 366
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-174-590-366

Query Match
 Best Local Similarity 100.0%; Score 1301; DB 14; Length 243;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQAKLREVEVDLYNGMCLQGPA 60
 DB 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQAKLREVEVDLYNGMCLQGPA 60
 QY 61 GVPGRDGPANVIGTPIGRDGFKEGKEGECLEBSFEESWTPTYKQCSWSLNYGIDL 120
 DB 61 GVPGRDGPANVIGTPIGRDGFKEGKEGECLEBSFEESWTPTYKQCSWSLNYGIDL 120
 QY 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCAGPLPIEATITVDQ 180
 DB 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCAGPLPIEATITVDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 11
 US-10-176-758-366
 Sequence 366, Application US/10176758
 Publication No. US20030008353A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jlan
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 US-10-176-758-366

APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C104
 CURRENT APPLICATION NUMBER: US/10/176,758
 PRIOR FILING DATE: 2002-06-21
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 366
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-758-366

Query Match
 Best Local Similarity 100.0%; Score 1301; DB 14; Length 243;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQAKLREVEVDLYNGMCLQGPA 60
 DB 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQAKLREVEVDLYNGMCLQGPA 60
 QY 61 GVPGRDGPANVIGTPIGRDGFKEGKEGECLEBSFEESWTPTYKQCSWSLNYGIDL 120
 DB 61 GVPGRDGPANVIGTPIGRDGFKEGKEGECLEBSFEESWTPTYKQCSWSLNYGIDL 120
 QY 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCAGPLPIEATITVDQ 180
 DB 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCAGPLPIEATITVDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 12
 US-10-175-737-366
 Sequence 366, Application US/10175737
 Publication No. US20030013153A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jlan
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C50
 CURRENT APPLICATION NUMBER: US/10/175,737
 PRIOR FILING DATE: 2002-06-19
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 366
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-175-737-366

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQGRA 60
DB 1 MRPGPASPQRRLGILLILLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQGRA 60
QY 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKRSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSPLEAIITLYDQ 180
DB 121 GKIACTFTKRSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSPLEAIITLYDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 13
US-10-063-616-122
; Sequence 122, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-122

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQGRA 60
DB 1 MRPGPASPQRRLGILLILLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQGRA 60
QY 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKRSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSPLEAIITLYDQ 180
DB 121 GKIACTFTKRSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSPLEAIITLYDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

DB 241 LPK 243

RESULT 14
US-10-174-581-366
; Sequence 366, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/174, 581
; CURRENT FILING DATE: 2002-06-18
; Prior Application Number: 10/052586
; Prior Filing Date: 2002-01-15
; Prior Application Number: 60/059263
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/059266
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/062250
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063120
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063121
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063486
; Prior Filing Date: 1997-10-21
; Prior Application Number: 60/063540
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063541
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063544
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063564
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063734
; Prior Filing Date: 1997-10-29
; Prior Application Number: 60/063870
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/065311
; Prior Filing Date: 1997-11-13
; Prior Application Number: 60/066120
; Prior Filing Date: 1997-11-21
; Prior Application Number: 60/066466
; Prior Filing Date: 1997-11-24
; Prior Application Number: 60/066772
; Prior Filing Date: 1997-11-24
; Prior Application Number: 60/069335
; Prior Filing Date: 1997-12-11
; Prior Application Number: 60/069425
; Prior Filing Date: 1997-12-12
; Prior Application Number: 60/069870
; Prior Filing Date: 1997-12-17
; Prior Application Number: 60/068017
; Prior Filing Date: 1997-12-18
; Prior Application Number: 60/07450
; Prior Filing Date: 1998-03-10
; Prior Application Number: 60/077632
; Prior Filing Date: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
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 PRIOR FILING DATE: 1998-05-07
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
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 PRIOR FILING DATE: 1998-05-15
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086023
 PRIOR FILING DATE: 1998-05-18
 PRIOR APPLICATION NUMBER: 60/086392
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086486
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087098
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087208

PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
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 PRIOR FILING DATE: 1998-06-09
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 PRIOR FILING DATE: 1998-06-10
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RESULT 15

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/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C68
/ CURRENT APPLICATION NUMBER: US/10/176,483
/ CURRENT FILING DATE: 2002-06-20
/ Prior application removed - See file wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 366
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-176-483-366
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DB 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCORWYFTFNGAECSGPLPIEAIYYLDQ 180
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QY 241 LPK 243
DB 241 LPK 243
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Search completed: December 25, 2004, 05:29:47
Job time: 73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 02:24:05 ; Search time 77 Seconds
(without alignments)
1132.094 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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 PA (GENE) GENENTECH INC.
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 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX WPI, 2000-237871/20.
 DR N-PSDB; AAA37144.
 DR XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 12; Fig 246; 773p; English.
 PS
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
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XX 09-MAR-2000.
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PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108856P.
PR 18-NOV-1998; 98US-0108904P.
XX
XX (GETH ) GENENTECH INC.
XX
```

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
 XX WPI; 2000-237871/20.
 DR N-PSDB; AAA37123.
 XX

PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 XX molecule inhibitors of the relevant receptor/ligand interactions.
 XX

PS Claim 12; Fig 204; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR
 CC primers and hybridization probes used in the isolation of the PRO
 CC polypeptides from the present invention

SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 3; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121; Mismatches 0; Gaps 0;
 Matches 243; Conservative 0; Indels 0;

QY 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEPKGKQKQLRQREVVDLYNMGCLQGPA 60
 DB 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEPKGKQKQLRQREVVDLYNMGCLQGPA 60
 QY 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECLERESFEESWTPTYKQCSWSSLYNGIDL 120
 DB 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECLERESFEESWTPTYKQCSWSSLYNGIDL 120
 QY 121 GKIAECTFTKRSNSALRYLFSGSLRLKCRNACCQRYWTFENGACSGPLPIEAIYYLDQ 180
 DB 121 GKIAECTFTKRSNSALRYLFSGSLRLKCRNACCQRYWTFENGACSGPLPIEAIYYLDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDPYPRGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDPYPRGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 3

ID AAB66190 standard; protein; 243 AA.
 XX
 AC AAB66190;

DT 02-APR-2001 (first entry)

DE Protein of the invention #102.

KW Secreted; transmembrane; gene therapy.

OS Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000WO-US004342.

XX 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.

PA (CETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillen KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WT;

XX WPI; 2001-071395/08.

DR

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 XX therapy.

XX

PS Claim 1; Fig 204; 787pp; English.

CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes in chromosome and gene mapping and in the generation of anti-
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy

SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121; Mismatches 0; Gaps 0;
 Matches 243; Conservative 0; Indels 0;

QY 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEPKGKQKQLRQREVVDLYNMGCLQGPA 60
 DB 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEPKGKQKQLRQREVVDLYNMGCLQGPA 60
 QY 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECLERESFEESWTPTYKQCSWSSLYNGIDL 120
 DB 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECLERESFEESWTPTYKQCSWSSLYNGIDL 120
 QY 121 GKIAECTFTKRSNSALRYLFSGSLRLKCRNACCQRYWTFENGACSGPLPIEAIYYLDQ 180
 DB 121 GKIAECTFTKRSNSALRYLFSGSLRLKCRNACCQRYWTFENGACSGPLPIEAIYYLDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDPYPRGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDPYPRGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 4

ID AAB66211 standard; protein; 243 AA.
 XX
 AC AAB66211;

DT 02-APR-2001 (first entry)

DE Protein of the invention #123.

KW Secreted; transmembrane; gene therapy.

OS Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

expression in the test sample indicates the presence of a tumour in the CC mammal. Mammals include dogs, cats, cattle, horses, sheep, goats CC and rabbits but are preferably human. The polypeptides can be used to CC stimulate tumour necrosis factor (TNF) alpha release from human blood, CC when contacted with it. A specific polypeptide can be used to stimulate CC the proliferation or differentiation of chondrocyte cells. The PRO CC proteins can be used to determine the presence of tumours and also CC susceptibility to tumour development, particularly adrenal, lung, colon CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids CC can be used for genetic analysis of individuals with genetic disorders XX

Sequence 243 AA:

Query Match

| | | | | |
|-----------------------|----------------|--------------------|----------|------------|
| Query Match | 100.0% | Score 1301 | DB 4 | Length 243 |
| Best Local Similarity | 100.0% | Pred. No. 3.2e-121 | | |
| Matches 243 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

| | | | | |
|----|-----|-----------------------|--|-----|
| QY | 1 | MRPGGPAASPORTRL | LLLLLLLLLLLLLQLPAPSSASHTPKQKQAKOLRQREVVLDLYNGMCLQSPA | 60 |
| Db | 1 | MRPGGPAASPORTRL | LLLLLLLLLLLLLQLPAPSSASHTPKQKQAKOLRQREVVLDLYNGMCLQSPA | 60 |
| QY | 61 | GVRPRDSSPGANVTPGTPGIP | PGRDGPKKEKCECLRESEESWTPMYKQCSMSLNYGIDL | 120 |
| Db | 61 | GVRPRDSSPGANVTPGTPGIP | PGRDGPKKEKCECLRESEESWTPMYKQCSMSLNYGIDL | 120 |
| QY | 121 | GKTAECTFTKRSNSALRVLP | SGSLRLKCRNAACQRMFTFNGACESGPLEIIEATIIYDQ | 180 |
| Db | 121 | GKTAECTFTKRSNSALRVLP | SGSLRLKCRNAACQRMFTFNGACESGPLEIIEATIIYDQ | 180 |
| QY | 181 | GSEPMNSTINIHR | TSVEGLCEGIGAGLVDAIVWGTCSDVPKXDASTGMNSVRIITEE | 240 |
| Db | 181 | GSEPMNSTINIHR | TSVEGLCEGIGAGLVDAIVWGTCSDVPKXDASTGMNSVRIITEE | 240 |
| QY | 241 | LPRK | 243 | |
| Db | 241 | LPRK | 243 | |

RESULT 6
AAB87586
ID AAB87586 standard; protein; 243 AA.
XX

| | | |
|----|-------------|-----------------|
| PR | 15-SEP-1999 | 99WC-US020111 |
| PR | 01-SEP-1999 | 99WC-US021090 |
| PR | 07-DEC-1999 | 99WC-0169495P |
| PR | 09-DEC-1999 | 99US-0170262P |
| PR | 11-JAN-2000 | 2000US-0175461P |
| PR | 16-FEB-2000 | 2000WC-US004341 |
| PR | 18-FEB-2000 | 2000WC-US004342 |
| PR | 22-FEB-2000 | 2000WC-US004414 |
| PR | 01-MAR-2000 | 2000WC-US005601 |
| PR | 03-MAR-2000 | 2000US-0187302P |
| PR | 21-MAR-2000 | 2000US-0191070P |
| PR | 30-MAR-2000 | 2000WC-US008439 |
| PR | 25-APR-2000 | 2000US-019397P |
| PR | 22-MAY-2000 | 2000WC-US014042 |

PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH) GENENTECH INC.
XX

PT biology, including use as hybridization probes, and in chromosome and gene mapping.

PS Claim 12; Fig 122; 278pp; English.
XX

The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular or anti-PRO antibodies. The PRO protein has been coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

Sequence 243 AA;

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1301; | DB 4; | Length 243; |
| Best Local Similarity | 100.0%; | Pred. No. 3.2e-121; | | |
| Matches 243; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

[illegible]

RESULT 7
BG95911
X ABG95911 standard; protein; 243 AA.

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XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089523P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100629P.
PR 16-SEP-1998; 98US-0100630P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023322.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 10-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

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PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WT,
XX
XX MPI; 2002-731348/79.
XX N-PSDB; ABS74438.
XX
XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX Claim 20; Fig 122; 399pd; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG55851-ABG55934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, G/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample.
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The B, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC invention represents a novel secreted or transmembrane protein of the
CC
XX
XX Sequence 243 AA:
SQ
Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3,28-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPGPASPRLRGLLLLLQLPAPSSASIRPKGKAKOLRQREVDLYNMGMLQGA 60
DB 1 MRPGPASPRLRGLLLLLQLPAPSSASIRPKGKAKOLRQREVDLYNMGMLQGA 60
QY 61 GVPRGDSFGANVIRPTGIPGRDGFKEBKEGCLRESFEESWTPYVKQCSWSLNYGIDL 120

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DB 61 GVGGRDSSPGANVITGTPGIPGRDGFGEKGECLRSFESSWTPNPKQCSMSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSSGLLCKNACCCORWYTFNGAECGSLPTEAIYYLDO 180
 DB 121 GKIAECTFTKRSNSALRVLFSSGLLCKNACCCORWYTFNGAECGSLPTEAIYYLDO 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 8
 ABB84939
 ID ABB84939 standard; protein; 243 AA.
 AC ABB84939;
 DT 16-MAY-2002 (first entry)
 DE Human PRO1550 protein sequence SEQ ID NO:246.
 XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KM vunerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping.
 OS Homo sapiens.
 XX
 OS
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 PF 20-JUN-2001; 2001WO-US019692.
 XX

23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 28-JUL-2000; 2000US-0220710P.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-0222695P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023528.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US019692.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00766498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001US-00802706.
 PR 09-MAR-2001; 2001US-00808689.
 PR 14-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00828366.
 PR 05-APR-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 10-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 FA (BETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A,
 PI Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX
 DR WPI, 2002-090516/12.
 DR N-PSDB; ABL88194.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 XX infarction), endothelial or angiogenic disorders in a mammal.
 PS Claim 11; Fig 246; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vunerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABB88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQKQRLRREYVDLYNKCQOGPA 60
 DB 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQKQRLRREYVDLYNKCQOGPA 60
 QY 61 GVGGRDSSPGANVITGTPGIPGRDGFGEKGECLRSFESSWTPNPKQCSMSLNYGIDL 120
 DB 61 GVGGRDSSPGANVITGTPGIPGRDGFGEKGECLRSFESSWTPNPKQCSMSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSSGLLCKNACCCORWYTFNGAECGSLPTEAIYYLDO 180
 DB 121 GKIAECTFTKRSNSALRVLFSSGLLCKNACCCORWYTFNGAECGSLPTEAIYYLDO 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 9
 AAE20462
 ID AAE20462 standard; protein; 243 AA.
 AC AAE20462;
 DT 01-JUL-2002 (first entry)
 DE Human tumour-associated antigenic target-170 (TA1170) protein.
 XX

01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.

(GERTH) GENENTECH INC.
(BAKER) BAKER K P.
(FERR) FERRARA N.
(GERB) GERBER H.
(GERR) GERRITSEN M E.
(GODD) GODDARD A.
(GODD) GODDARD P J.
(GURN) GURNEY A L.
(HILL) HILLAN K J.
(MARS) MARSTERS S A.
(PANU) PAN J.
(PAON) PAONI N F.
(STEP) STEPHAN J F.
(WATA) WATANABE C K.
(WILL) WILLIAMS P M.
(WOOD) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, WPI; 2002-171999/22.
N-PSDB; ABL95683.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
Claim 11; Fig 246; 567PD; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including a hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention

Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3, 2e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPGPASPQRRLGRLILLLILQLPAPSSASEIPKQKQKQRLRQREVDVLYNMGCLQGPA 60
1 MRPGPASPQRRLGRLILLLILQLPAPSSASEIPKQKQKQRLRQREVDVLYNMGCLQGPA 60
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKECLRSFESWTPTYKQCSMSLNYGIDL 120
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKECLRSFESWTPTYKQCSMSLNYGIDL 120
121 GKIACTFTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFGAGCSGPLEIAIITYDQ 180
121 GKIACTFTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFGAGCSGPLEIAIITYDQ 180
181 GSPENNSTINIRTSVSGLCGIGAGLVDAIWTGTSYDPKGDASTGMSVSRITIEE 240
181 GSPENNSTINIRTSVSGLCGIGAGLVDAIWTGTSYDPKGDASTGMSVSRITIEE 240
241 LPK 243
241 LPK 243

RESULT 11
ABP68636
ID ABP68636 standard; protein; 243 AA.

AC ABP68636;
14-JAN-2003 (first entry)
Human pancreatic cancer expressed protein SEQ ID NO 4559.

Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytotoxic; tumour.
Homo sapiens.
WO200260317-A2.
08-AUG-2002.

30-JAN-2002; 2002WO-US002781.
30-JAN-2001; 2001US-0265305P.
31-JAN-2001; 2001US-0265682P.
09-FEB-2001; 2001US-0267568P.
21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313998P.
27-NOV-2001; 2001US-0333626P.

(CORI-) CORIYA CORP.
Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
WPI; 2002-627435/67.
N-PSDB; ABV99144.

New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosis, preventing and/or treating cancer, particularly pancreatic cancer.

Claim 2; SEQ ID NO 4559; 300bp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (1) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences that hybridize to (a) under moderate stringency conditions; (d) sequences having at least 75% or 90% identity to (a); or (e) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridization, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3, 2e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPGPASPQRRLGRLILLLILQLPAPSSASEIPKQKQKQRLRQREVDVLYNMGCLQGPA 60
1 MRPGPASPQRRLGRLILLLILQLPAPSSASEIPKQKQKQRLRQREVDVLYNMGCLQGPA 60
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKECLRSFESWTPTYKQCSMSLNYGIDL 120
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKECLRSFESWTPTYKQCSMSLNYGIDL 120
121 GKIACTFTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFGAGCSGPLEIAIITYDQ 180
121 GKIACTFTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFGAGCSGPLEIAIITYDQ 180

DB 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYTFNGAECSGLPIEAIITLQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
QY 241 LPK 243
DB 241 LPK 243
RESULT 12
ABG78938
ID ABG78938 standard; protein; 243 AA.
AC ABG78938;
XX 15-NOV-2002 (first entry)
DT 15-NOV-2002 (first entry)
XX
DE Human breast tumour polypeptide #29.
XX
KW Human; breast tumour protein; breast cancer; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2002085998-A1.
XX
PD 04-JUL-2002.
XX
PF 13-APR-2001; 2001US-00834759.
XX
PR 28-DEC-1998; 98US-00223575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX
PA (CORI-) CORIXA CORP.
XX
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI Henderson RA;
XX
XX MPI; 2002-635657/68.
DR N-PSDB; ABS64028, ABS64029.
XX
PT Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in a
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX
PS Claim 2; Page 235-236; 247pp; English.
XX
CC The invention relates to an isolated breast tumour polynucleotide and the
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC detecting the presence of breast cancer in a patient, and in
CC pharmaceutical compositions for treating breast cancer. The sequences are
CC useful for stimulating an immune response in a patient and can therefore
CC be used in production of vaccines. The sequences are also useful for
CC detecting the presence of a cancer in a patient, by obtaining a
CC biological sample from the patient, contacting the biological sample with
CC a composition of the invention and detecting the amount of polynucleotide
CC that hybridizes to the sample. This sequence represents a human breast
CC tumour polypeptide of the invention
XX
SQ Sequence 243 AA;

QY 1 MRPGPAPSPORLRLGLLLLLQLPAPSSASEIPKQKAKOLROREVVDLYNGMCLQGA 60
DB 1 MRPGPAPSPORLRLGLLLLLQLPAPSSASEIPKQKAKOLROREVVDLYNGMCLQGA 60
QY 61 GVPGRDPSGANVIRPOTPGIPGRDPFKGEKGECLAESFEESWTPNVKQCSWSLNYGIDL 120
DB 61 GVPGRDPSGANVIRPOTPGIPGRDPFKGEKGECLAESFEESWTPNVKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYTFNGAECSGLPIEAIITLQ 180
DB 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYTFNGAECSGLPIEAIITLQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
QY 241 LPK 243
DB 241 LPK 243
RESULT 13
ABUS8582
ID ABUS8582 standard; protein; 243 AA.
XX
AC ABUS8582;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #183.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADPRT;
XX antibody-dependent enzyme mediated prodrug therapy.
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.

PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1301; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.2e-121; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQALRQREVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQALRQREVDLYNGMCLQGPA 60
QY 61 GVPGRDGSFGANYIPGTGIPGRDGFKEGKECLRESFESWTPTNTKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANYIPGTGIPGRDGFKEGKECLRESFESWTPTNTKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCQRMWFTFNGAECGFLPIEATITLIDQ 180
DB 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCQRMWFTFNGAECGFLPIEATITLIDQ 180
QY 181 GSPENNSTINIRHTSVBGLCEGIGAGLYDVVAIWGTCSDYPRGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIRHTSVBGLCEGIGAGLYDVVAIWGTCSDYPRGDASTGMNSVSRITIEE 240
QY 241 LFK 243
DB 241 LFK 243

Search completed: December 25, 2004, 05:25:48
Job time : 80 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 05:09:56 ; Search time 96 Seconds

(without alignments)
1456.417 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPAPSPQRLGILLLL.....GDPSTGMSVSRRIIEBLPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1301 | 100.0 | 243 | 2 | Q6UW91 |
| 2 | 1301 | 100.0 | 243 | 2 | AAG89273 |
| 3 | 1294 | 99.5 | 243 | 2 | Q96C68 |
| 4 | 1266 | 93.5 | 245 | 2 | Q8C608 |
| 5 | 1201 | 92.3 | 245 | 2 | Q9D1D6 |
| 6 | 1052 | 80.9 | 232 | 2 | Q81X63 |
| 7 | 132 | 10.1 | 565 | 2 | Q8K036 |
| 8 | 124.5 | 9.6 | 717 | 2 | Q9NQ52 |
| 9 | 122.5 | 9.4 | 246 | 1 | C1OC_MOUSE |
| 10 | 122.5 | 9.4 | 1472 | 2 | Q9Q2A0 |
| 11 | 120 | 9.2 | 287 | 2 | Q8CPR0 |
| 12 | 120 | 9.2 | 1752 | 2 | Q07265 |
| 13 | 119 | 9.1 | 289 | 2 | Q18799 |
| 14 | 118.5 | 9.1 | 358 | 2 | Q6MEY7 |
| 15 | 118.5 | 9.1 | 358 | 2 | CARF2862 |
| 16 | 118.5 | 9.1 | 1069 | 2 | Q6LAN8 |
| 17 | 118.5 | 9.1 | 1069 | 2 | CAAE7261 |
| 18 | 118.5 | 9.1 | 1461 | 2 | Q76045 |
| 19 | 118.5 | 9.1 | 1464 | 1 | CA11_HUMAN |
| 20 | 118.5 | 9.1 | 1464 | 2 | Q8NA73 |
| 21 | 118 | 9.1 | 291 | 2 | Q9NAR3 |
| 22 | 118 | 9.1 | 832 | 2 | Q96F77 |
| 23 | 118 | 9.1 | 1860 | 2 | Q812C6 |
| 24 | 117.5 | 9.0 | 540 | 2 | Q86V22 |
| 25 | 117.5 | 9.0 | 568 | 2 | Q8CD80 |
| 26 | 117.5 | 9.0 | 739 | 2 | Q70575 |
| 27 | 117.5 | 9.0 | 747 | 2 | Q6NWS7 |
| 28 | 117.5 | 9.0 | 747 | 2 | AA67716 |
| 29 | 117.5 | 9.0 | 751 | 2 | Q9R1N9 |
| 30 | 117 | 9.0 | 327 | 2 | Q01799 |
| 31 | 117 | 9.0 | 754 | 1 | CAS4_CANFA |

| | | | | | |
|----|-------|-----|------|---|------------|
| 32 | 117 | 9.0 | 1447 | 2 | Q6P4U1 |
| 33 | 117 | 9.0 | 1447 | 2 | Q6U1J5 |
| 34 | 117 | 9.0 | 1447 | 2 | AA63249 |
| 35 | 117 | 9.0 | 1447 | 2 | AA24536 |
| 36 | 117 | 9.0 | 1669 | 2 | Q9Q2S0 |
| 37 | 116 | 8.9 | 551 | 2 | Q6ZM13 |
| 38 | 116 | 8.9 | 551 | 2 | BAD18742 |
| 39 | 116 | 8.9 | 886 | 2 | Q9NUR7 |
| 40 | 116 | 8.9 | 888 | 2 | Q90796 |
| 41 | 116 | 8.9 | 1670 | 1 | CA34_HUMAN |
| 42 | 116 | 8.9 | 1685 | 1 | CAS4_HUMAN |
| 43 | 115.5 | 8.9 | 289 | 1 | Q077_HUMAN |
| 44 | 115.5 | 8.9 | 1075 | 2 | Q86X41 |
| 45 | 115.5 | 8.9 | 1336 | 2 | Q6RZ41 |

ALIGNMENTS

| RESULT 1 | ID | Q6UW91 | PRELIMINARY | PRT | 243 AA. |
|---------------------------|---|---|-------------|-----|---------|
| AC | Q6UW91 | | | | |
| DT | 05-JUL-2004 | (TREMBLrel. 27, Created) | | | |
| DT | 05-JUL-2004 | (TREMBLrel. 27, Last sequence update) | | | |
| DT | 05-JUL-2004 | (TREMBLrel. 27, Last annotation update) | | | |
| DE | CTHRC1 | | | | |
| GN | ORFName=UNQ762; | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_Taxid=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=22887296; PubMed=12975309; | | | | |
| RA | Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., | | | | |
| RA | Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., | | | | |
| RA | Huang A., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S., | | | | |
| RA | Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J., | | | | |
| RA | Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., | | | | |
| RA | Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., | | | | |
| RA | Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., | | | | |
| RA | Godowski P.; | | | | |
| RT | "The secreted protein discovery initiative (SPDI), a large-scale | | | | |
| RT | effort to identify novel human secreted and transmembrane proteins: a | | | | |
| RT | bioinformatics assessment." | | | | |
| RL | Genome Res. 13:2265-2270(2003). | | | | |
| DR | EMBL; AY358914; AAQ89273.1; - | | | | |
| DR | InterPro; IPR008161; Clg_helix. | | | | |
| DR | InterPro; IPR008160; Collagen. | | | | |
| DR | Prodom; PD000007; Clg_helix; 1. | | | | |
| KW | COLLAGEN. | | | | |
| SC | SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC030BC CRC64; | | | | |
| Query Match | 100.0%; Score 1301; DB 2; Length 243; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 6.5e-108; Mismatches 0; | | | | |
| Matches 243; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 1 | MRPGPAPSPQRLGILLLLQLPAPSASERIPKQKQAKQREBVVDLYNGMCLQSPA | 60 | | |
| DB | 1 | MRPGPAPSPQRLGILLLLQLPAPSASERIPKQKQAKQREBVVDLYNGMCLQSPA | 60 | | |
| QY | 61 | GVPGRDSPGANVITGTCIGIPGRDPFKGKGCLEBSEFTPTNYKQCSWSLNYGIDL | 120 | | |
| DB | 61 | GVPGRDSPGANVITGTCIGIPGRDPFKGKGCLEBSEFTPTNYKQCSWSLNYGIDL | 120 | | |
| QY | 121 | GKIARCTFTKMSNALTALVTFSGSLRLKCRNACCGRWTFPGARCSGGLPTEATITVLDQ | 180 | | |
| DB | 121 | GKIARCTFTKMSNALTALVTFSGSLRLKCRNACCGRWTFPGARCSGGLPTEATITVLDQ | 180 | | |
| QY | 181 | GSPENNSTINIRTSVEGLCEGIGAGLVDAIWIWGCSDPYKGDASTGMSVSRRIIEE | 240 | | |
| DB | 181 | GSPENNSTINIRTSVEGLCEGIGAGLVDAIWIWGCSDPYKGDASTGMSVSRRIIEE | 240 | | |

DB 241 LFK 243

RESULT 4

Q8CG08 PRELIMINARY; PRT; 245 AA.

AC Q8CG08; 01-MAR-2003 (TREMBLrel. 23, last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, last annotation update)

GN Name=Ctrcl;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY136824; AAN15748.1; -

DR GO; GO:0005737; Cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR008161; Clg helix.

DR InterPro; IPR008160; Collagen.

DR Pfam; PF01391; Collagen 1.

DR Prodom; PD000007; Clg_helix; 1.

KW Collagen.

SEQUENCE 245 AA; 26424 MW; 2296FD6DCDBA21F2 CRC64;

Query Match 93.5%; Score 1216; DB 2; Length 245;

Best Local Similarity 94.3%; Pred. No. 2.6e-100; Matches 231; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 MRPGPAASPPRLRG-LTLLTLLLPAPSSASEIPKQKQQLRQREVVDLYNGMCLOG 58

DB 1 MRPGPAASPPRLRG-LTLLTLLLPAPSSASEIPKQKQQLRQREVVDLYNGMCLOG 60

QY 59 PAGVPGRDGSPGANYIPGTPIPGRDGFGKGEKCELRSEFESWTPNYKQCSWSSINYG 118

DB 61 PAGVPGRDGSPGANYIPGTPIPGRDGFGKGEKCELRSEFESWTPNYKQCSWSSINYG 120

QY 119 DLGKIAECTFTMRNSALRVFSGSLRCKRNACCQRYFTFNAGECGPIPIAIIYL 178

DB 121 DLGKIAECTFTMRNSALRVFSGSLRCKRNACCQRYFTFNAGECGPIPIAIIYL 180

QY 179 DQSGEMNSTINIHRTSSVEGLCEGIGAGLVVAIVWGTCSDPYKGDASTGNNVSRIIT 238

DB 181 DQSGEMNSTINIHRTSSVEGLCEGIGAGLVVAIVWGTCSDPYKGDASTGNNVSRIIT 240

QY 239 EELPK 243

DB 241 EELPK 245

RESULT 5

Q9DID6 PRELIMINARY; PRT; 245 AA.

AC Q9DID6; 01-JUN-2001 (TREMBLrel. 17, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)

DE 01-JUN-2003 (TREMBLrel. 24, last annotation update)

DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014807 product:hypothetical collagen triple helix repeat containing protein, full insert sequence.

GN Name=Ctrcl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=20499374; PubMed=11042159;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai Y., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arahawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito R., Saito C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK003674; BAB22930.1; -

DR MGD; MGI:1915838; Ctrcl.

DR GO; GO:0005737; Cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR008161; Clg helix.

DR InterPro; IPR008160; Collagen.

DR Pfam; PF01391; Collagen 1.

DR Prodom; PD000007; Clg_helix; 1.

KW Collagen; Hypothetical protein.

SEQUENCE 245 AA; 26460 MW; 14951B87D8181A08 CRC64;

Query Match 92.3%; Score 1201; DB 2; Length 245;

Best Local Similarity 93.1%; Pred. No. 5.6e-99; Matches 228; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

| | Query Match | 80.9%; | Score 1052; | DB 2; | Length 232; |
|----|--|--------------|--------------------|----------------|--------------------|
| | Best Local Similarity | 83.1%; | Pred. No. 1,1e-85; | | |
| | Matches | Conservative | 8; | Mismatches 19; | Indels 14; Gaps 2; |
| QY | 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQAKQALRQREVVDLYNGMGLQSPA | 1 | | 60 | |
| Db | 1 MWPFRSRT-VKLREKTVSRKLENNGPSAFGLIGK-----YNGMLQSGPA | 1 | | 46 | |
| QY | 61 GVPGGDGPAGAVVIGTPGIPGRDQPKFKGKGCLEASFESWTPTYKOCSSWLSNYGIDL | 61 | | 120 | |
| Db | 47 GVPGGDGPAGAVVIGTPGIPGRDQPKFKGKGCLEASFESWTPTYKOCSSWLSNYGIDL | 47 | | 106 | |
| QY | 121 GKIAECTTKKRSNALSRLVLPFSGSLRLCRNACCQRMVFTFENGACSGPLPLEAIYYDQ | 121 | | 180 | |
| Db | 107 GKIAECTTKKRSNALSRLVLPFSGSLRLCRNACCQRMVFTFENGACSGPLPLEAIYYDQ | 107 | | 166 | |
| QY | 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTSDDYPKQDASTGMSVSRIITIEE | 181 | | 240 | |
| Db | 167 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTSDDYPKQDASTGMSVSRIITIEE | 167 | | 226 | |
| QY | 241 LP 242 | 241 | | | |
| Db | 227 LP 228 | 227 | | | |

```

Query Match      10.1%; Score 132; DB 2; Length 565;
Best Local Similarity 33.9%; Pred. No. 0.0043;
Matches 38; Conservative 13; Mismatches 35; Indels 26; Gaps 6

QY 27 PPSASRI---PKGKQKALRREVEVDLYNG-----NCLQSPAGVPRDSSPCA 71
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 PQAAGQGQSPSGKX-AKGEPRKGEVND-YNSINIEALQELRTALMGPPQLPQGTSPGP 450
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 72 NVIPGTP-----GIQRDGFKGECECTAESFEESFTPVYKOCSSWSLYNG 117
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 ---PGRPGRGELIGLPGPHGDHDKGRGRKRGDAGCAGSSSTTRPKGMASSNEG 499
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

| RESULT 8 | |
|----------------|---|
| Q9NO52 | PRELIMINARY; |
| ID | PRT; 717 AA. |
| Q9NO52 | |
| DT 01-OCT-2000 | (TRENDArel. 15, Created) |
| DT 01-OCT-2000 | (TRENDArel. 15, Last sequence update) |
| DT 01-MAR-2004 | (TRENDArel. 26, Last annotation update) |

```

DE Type XIII collagen.
GN Name=COLXIII.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Snellman A., Tu H., Vaelsaenen T., Kvist A.P., Huhala P.,
RA Pihlajaniemi T.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293624; CAC00688.1; -.
DR Genew; HGNC:2190; COL13A1.
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0006817; P-phosphate transport; IEA.
DR InterPro; IPR008161; C1q helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 9.
DR Prodom; PD000007; C1q_helix; 3.
KW Collagen.
SQ SEQUENCE 717 AA; 69964 MW; A311E9C7D3E87577 CRC64;

Query Match 9.6%; Score 124.5; DB 2; Length 717;
Best Local Similarity 42.1%; Pred. No. 0.026;
Matches 32; Conservative 8; Mismatches 17; Indels 19; Gaps 4;

QY 34 PGGKQKAGLRQREVDVLYNG-----MCLQGPAGVPRDGFPGANVLP-----G 76
DB 431 PGG-SGEGEKEMVD-YNGNINELQEIETRLALMGPGLPGQIGPPAGIPGGKGEIG 488
QY 77 TPGIPGRDGFKEGKE 92
DB 489 LPGPFGHDEKGPGRK 504

RESULT 9
C1QC_MOUSE STANDARD; PRT; 246 AA.
ID C1QC_MOUSE
AC 002105;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Complement C1q subcomponent, C chain precursor.
GN Name=C1qg; Synonym=C1qc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ICR; TISSUE=Macrophage;
RC MEDLINE=9301118; PubMed=1396691;
RA Petry F., Reid K.B.M., Loos M.;
RT "Isolation, sequence analysis and characterization of cDNA clones
RT coding for the C chain of mouse C1q. Sequence similarity of complement
RT subcomponent C1q, collagen type VIII and type X and precerebellin.",
RL Eur. J. Biochem. 209:129-134(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c; TISSUE=Liver;
RC MEDLINE=96186528; PubMed=8606057;
RA Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;
RT "The mouse C1q genes are clustered on chromosome 4 and show
RT conservation of gene organization.",
RL Immunogenetics 43:370-376(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Cavaletto T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: C1q associates with the proenzymes C1r and C1s to yield
CC C1, the first component of the serum complement system. The
CC collagen-like regions of C1q interact with the C1(2+)-dependent
CC C1r(2)C1s(2) proenzyme complex, and efficient activation of C1
CC takes place on interaction of the globular heads of C1q with the
CC Fc regions of IgG or IgM antibody present in immune complexes.
CC -1- SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q, R
CC and S in the molar ratio of 1:2:2. C1q subcomponent is composed
CC of nine subunits, six of which are disulfide-linked dimers of the
CC A and B chains, and three of which are disulfide-linked dimers of
CC the C chain.
CC -1- SIMILARITY: Contains 1 C1q domain.
CC -1- SIMILARITY: Contains 1 collagenous domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X66295; CAA46993.1; -.
DR EMBL; X92960; CAA63535.1; -.
DR EMBL; BC054443; AAH54443.1; -.
DR PIR; S29328; S29328.
DR HSSP; 060994; 1C28.
DR MGD; MGI:88225; C1qg.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR008161; C1q_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF-like.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR Prodom; PD000007; C1q_helix; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen; Complement pathway; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Signal.
FT FT SIGNAL 1 29
FT CHAIN 30 246
FT DOMAIN 32 113
FT DOMAIN 114 246
FT DISULFID 33 33
FT MOD_RES 37 37 Hydroxyproline (By similarity).
FT MOD_RES 40 40 Hydroxyproline (By similarity).
FT MOD_RES 43 43 Hydroxyproline (By similarity).
FT MOD_RES 61 61 Hydroxyproline (By similarity).
FT MOD_RES 64 64 Hydroxyproline (By similarity).
FT MOD_RES 73 73 5-hydroxylysine (By similarity).
FT MOD_RES 76 76 5-hydroxylysine (By similarity).
FT MOD_RES 79 79 Hydroxyproline (By similarity).
FT MOD_RES 82 82 Hydroxyproline (By similarity).
FT MOD_RES 97 97 Hydroxyproline (By similarity).
FT MOD_RES 100 100 Hydroxyproline (By similarity).
FT MOD_RES 106 106 Hydroxyproline (By similarity).

```

FT MOD RES 109 109 Hydroxyproline (By similarity).
SQ SEQUENCE 246 AA; 25966 MW; 2F79BA1274BCB8E0 CRC64;
Query Match
Best Local Similarity 9.4%; Score 122.5; DB 1; Length 246;
Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;
QY 5 GPPASPORLRLGLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGAPGVP 64
DB 4 GPCQPCQCGCLLLFLPLPLRSQS-----AGCGIGMGMPGAPG 47
QY 65 RDGS---PGANVPGTGTGIRGRGPKKEKE 92
DB 48 KQGHDLGQPKGEBGIPAVPTGQPKQKGE 78
RESULT 10
ID 0902AO PRELIMINARY; PRT; 1472 AA.
AC 0902AO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Collagen type XX alpha 1 precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21303548; PubMed=11274142;
RA Koch M., Foley J.E., Hahn R., Zhou P., Burgess R.E., Gerecke D.R.,
RT Gordon M.K.;
RT "alpha 1(X) collagen, a new member of the collagen subfamily, fibril-
associated collagens with interrupted triple helices";
RL J. Biol. Chem. 276:23120-23126(2001).
DR HSP; P56199; I0C5.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008985; Cora_like_1ec_g1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01391; Collagen_4.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR PRODOM; PD000007; Clg_helix; 4.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS50853; FN3; 6.
DR PROSITE; PS50234; VWA; 1.
KM Collagen; Signal.
FT SIGNAL 1 28 Potential.
SQ SEQUENCE 1472 AA; 156903 MW; 536161579C56EFD CRC64;
Query Match
Best Local Similarity 9.4%; Score 122.5; DB 2; Length 1472;
Matches 37; Conservative 7; Mismatches 27; Indels 39; Gaps 6;
QY 3 PGGPASPRLRLGLLLLLQLP-----APSSASRI-----PKGKQALRQREV 47
DB 1161 PGGPASPRLRLGLLLLLQLP-----APSSASRI-----PKGKQALRQREV 47
QY 48 VLYNGMCLQGAPGVP-----GRDGPANVPGTGTGIRGRDGPKEKE 91

DB 1208 -----GITTIQGVPPGIKKEKGTGSPMGQIGPVGAGPGRDLQAGAKG 1252
RESULT 11
ID 08CFRO PRELIMINARY; PRT; 287 AA.
AC 08CFRO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Clg-like.
GN Name=BC040774.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932;
RA Strusberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshimiyuki S., Carninci P., Prange C.,
RA Rana S.A., Loquellano N.A., Peters G.J., Abramson K.J., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC040774; AAR40774.1; -.
DR HSP; O60994; 1C28.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clg.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clg; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KM Collagen.
FT SIGNAL 1 287 AA; 29292 MW; 8FF89EC1C7420415 CRC64;
SQ SEQUENCE 287 AA; 29292 MW; 8FF89EC1C7420415 CRC64;
Query Match
Best Local Similarity 9.2%; Score 120; DB 2; Length 287;
Matches 42; Conservative 10; Mismatches 57; Indels 12; Gaps 4;
QY 27 PSSASRIPKGKQALRQREV-DIYNG---MCLQGAPGVPGRDGPANVPGTGTGIR 82
DB 44 PAKAKAPPPGPSTAL---EYWDLSANPPPPFQGGPGRGKGPGRGPPGP 100
QY 83 RGFKEKGECLRESEFSWTPNYKQGSWSLNYGIDLGKIAECTPTKMRNSALRLVLS 142
DB 101 PGPPEKEDSGRPL-----PGLQLTLSAAGGVVSGGTGGGDTGEVTSLSAIFS 155

QY 143 G 143
DB 156 G 156

RESULT 12

Q07265 PRELIMINARY; PRT; 1752 AA.

ID 007265
AC 007265;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE 3 alpha procollagen.
GN Name=COL3A1alpha;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93186842; PubMed=8444899;
RA Exposito J.-Y., D'Alessio M., Di Liberto M., Ramirez F.;
RT "Complete primary structure of a sea-urchin type IV collagen and
RT analysis of the 5' end of its gene."
RL J. Biol. Chem. 268:5249-5254(1993).
DR EMBL; L02917; AAA30039.1; -.
DR HSSP; P02462; 1L11.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001442; Procollagen_C.
DR Pfam; PF01413; C4; 2.
DR Pfam; PF01391; Collagen; 25.
DR SMART; SM00111; C4; 2.
DR Collagen.
KW SEQUENCE 1752 AA; 170210 MW; 1AB5AAA21569346D CRC64;

Query Match 9.2%; Score 120; DB 2; Length 1752;

Best Local Similarity 22.4%; Pred. No. 0.19; Matches 46; Conservative 20; Mismatches 61; Indels 78; Gaps 9;

QY 3 PGPASAPQRLRLQLLLQLLPASSASIRPKGKQKQALRQREVVLDYNGMCLQGPAV 62
DB 1453 PGPSPRDRG-----PGPQ3-----PPG-----LTGDKGT 1477
QY 63 PGRDGSFGANVIRPTGIPGRDGFKEKGECLRESF-----ESWT 103
DB 1478 FGVQGNFVSGVGEFELKQSGFRGNGQPPGPFPTGTGEGAGIRGSSGPFITTHSOT 1537
QY 104 PNYKQ-----SW-----SSLNVGIDLGKIAECTFTMRNSALRVLFSSLR 147
DB 1538 TSIPQCPQGTAKMHWGYSLLFVQGNRGGHGDLGKQSGC-----LKRFTMPFLFC-NINN 1592
QY 148 KCRNACCQRRYFTFNAGECGSLPI 172
DB 1593 VCHVASRNDYSYWLSTTE---PMPM 1614

RESULT 13

Q18799 PRELIMINARY; PRT; 289 AA.

ID 018799
AC 018799;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein C53B4.5.
GN Name=C53B4.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Petodermidae; Caenorhabditis.

OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Berke M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z68215; CAA92453.1; -.
DR F1R; T20177; T20177.
DR Wormpep; C53B4.5; C530391.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
KW Collagen; Hypothetical protein.
SQ SEQUENCE 289 AA; 28993 MW; 2999A3FF9CC0B044 CRC64;

Query Match 9.1%; Score 119; DB 2; Length 289;

Best Local Similarity 34.5%; Pred. No. 0.028; Matches 29; Conservative 5; Mismatches 20; Indels 30; Gaps 2;

QY 25 PAPSASIRPKGKQKQALRQREVVLDYNGMCLQGPAVGRDS-----P 69
DB 203 PPGSGSPRDRGQPS-----RGPAGQKQAGCGEKGANGEPGP 247
QY 70 GANVIRPTGIPGRDGFKEKGECC 93
DB 248 GRDQPRGRGPRGRDGFKEKGC 271

RESULT 14

Q6MEY7 PRELIMINARY; PRT; 358 AA.

ID 06MEY7
AC 06MEY7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFName=pc0138;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=null;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.U., Droge M., Frishman D.,
RA Rattai T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF22862.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
KW Hypothetical protein.
SQ SEQUENCE 358 AA; 37332 MW; 87419BD361E3D61B CRC64;

Query Match 9.1%; Score 118.5; DB 2; Length 358;

Best Local Similarity 28.1%; Pred. No. 0.04; Matches 45; Conservative 15; Mismatches 73; Indels 27; Gaps 5;

QY 34 PPKGKQALRQREVVLDYNGMCLQGPAVGRDGSFGANVIRPTGIPGRDGFKEKG-- 91

Db 136 PPGQATGATGPGPPGTGAGLTGTGATGTLTGADGPGADGMSGSKLT 195
 QY 92 -----ECLRESFEESWTPNY-----KQCSMSLNYGIDLGKIAE-----CTF 128
 Db 196 GATGTLGATGTLTGAGSPAGNNYFAYGIETGVSPPVNLSPDVCPILDGWRPTNTTF 255
 QY 129 TKMRSNSALRYLFGSGSLRLKCRNACCORWYFTFNAGACSG 168
 Db 256 TCKQTGIYL-VQVRGQFTLNVMDATCALM-ATFNGSQVEG 293

RESULT 15

CAF22862 PRELIMINARY; PRT; 358 AA.
 ID CAF22862
 AC CAF22862;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DE 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 GN Hypothetical protein.
 OS Parachlamydia sp. UME25.
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
 OX NCBI_TaxID=264201;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME25;
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rattei T., Mewes H., Wagner M.;
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing
 the evolutionary history of chlamydiae."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME25;
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rattei T., Mewes H., Wagner M.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BX908798; CAF22862.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 358 AA; 37332 MW; 87419BD361E3D61B CRC64;

Query Match 9.1%; Score 118.5; DB 2; Length 358;
 Best Local Similarity 28.1%; Pred.No.0.04; Mismatches 73; Indels 27; Gaps 5;

Matches 45; Conservative 15;
 QY 34 PKGKQKQLRQREVVDLYNGMCLQGPAGVGRDGSFGANVIRPTGIPGRDGFKEBKG-- 91
 Db 136 PPGQATGATGPGPPGTGAGLTGTGATGTLTGADGPGADGMSGSKLT 195
 QY 92 -----ECLRESFEESWTPNY-----KQCSMSLNYGIDLGKIAE-----CTF 128
 Db 196 GATGTLGATGTLTGAGSPAGNNYFAYGIETGVSPPVNLSPDVCPILDGWRPTNTTF 255
 QY 129 TKMRSNSALRYLFGSGSLRLKCRNACCORWYFTFNAGACSG 168
 Db 256 TCKQTGIYL-VQVRGQFTLNVMDATCALM-ATFNGSQVEG 293

Search completed: December 25, 2004, 05:28:01
 Job time : 100 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 03:56:15 / Search time 23 Seconds
(without alignments)
1016.551 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MKPGPAPASPORTLRLGLLTL.....GDASTGMSVSRILIEELPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------------|
| 1 | 122.5 | 9.4 | 246 | 2 | S29328 complement subcomp |
| 2 | 120 | 9.2 | 1752 | 2 | A45407 collagen alpha 3(I) |
| 3 | 119 | 9.1 | 289 | 2 | T20177 hypothetical prote |
| 4 | 118.5 | 9.1 | 1464 | 1 | CGH01S collagen alpha 1(I) |
| 5 | 117 | 9.0 | 327 | 2 | T29031 hypothetical prote |
| 6 | 117 | 9.0 | 754 | 2 | A55267 collagen alpha 5(I) |
| 7 | 116 | 8.9 | 888 | 2 | S28791 collagen alpha 1(X) |
| 8 | 116 | 8.9 | 1670 | 1 | CGH03B collagen alpha 3(I) |
| 9 | 115.5 | 8.9 | 1669 | 1 | CGH04B collagen alpha 1(I) |
| 10 | 115 | 8.8 | 1466 | 1 | CGH07L collagen alpha 1(I) |
| 11 | 115 | 8.8 | 1763 | 2 | S16366 collagen alpha 2(I) |
| 12 | 114.5 | 8.8 | 311 | 2 | T15268 hypothetical prote |
| 13 | 114 | 8.8 | 304 | 2 | T26185 hypothetical prote |
| 14 | 114 | 8.8 | 304 | 2 | T26184 hypothetical prote |
| 15 | 114 | 8.8 | 1691 | 1 | S22917 collagen alpha 5(I) |
| 16 | 113.5 | 8.7 | 300 | 2 | T24482 hypothetical prote |
| 17 | 113.5 | 8.7 | 920 | 2 | A45748 collagen alpha 1(V) |
| 18 | 113.5 | 8.7 | 1549 | 2 | I48103 type VII collagen |
| 19 | 113.5 | 8.7 | 1691 | 2 | CGH06B collagen alpha 6(I) |
| 20 | 113 | 8.7 | 2944 | 2 | AS4849 collagen alpha 1(V) |
| 21 | 112 | 8.6 | 178 | 2 | A39762 collagen alpha 1(X) |
| 22 | 112 | 8.6 | 325 | 2 | T18594 hypothetical prote |
| 23 | 111.5 | 8.5 | 428 | 2 | T24769 hypothetical prote |
| 24 | 111 | 8.5 | 245 | 1 | C1H0C complement subcomp |
| 25 | 111 | 8.5 | 358 | 2 | T26281 hypothetical prote |
| 26 | 110.5 | 8.5 | 298 | 2 | T27644 hypothetical prote |
| 27 | 110.5 | 8.5 | 310 | 2 | T29731 hypothetical prote |
| 28 | 110.5 | 8.5 | 458 | 2 | T31631 hypothetical prote |
| 29 | 110.5 | 8.5 | 671 | 1 | CGR1S collagen alpha 1(I) |

| | | | | | |
|----|-------|-----|------|---|----------------------------|
| 30 | 110.5 | 8.5 | 1453 | 2 | S21626 collagen alpha 1(I) |
| 31 | 110 | 8.5 | 298 | 2 | JCI448 collagen col-34 - |
| 32 | 110 | 8.5 | 299 | 2 | T29956 hypothetical prote |
| 33 | 110 | 8.5 | 1042 | 1 | CGCHS collagen alpha 1(I) |
| 34 | 110 | 8.5 | 1049 | 1 | CGS07S collagen alpha 1(I) |
| 35 | 110 | 8.5 | 1568 | 2 | T09074 semaphorin recepto |
| 36 | 110 | 8.5 | 1806 | 1 | CGH1E collagen alpha 1(X) |
| 37 | 109.5 | 8.4 | 177 | 2 | S37749 collagen alpha 2(X) |
| 38 | 109.5 | 8.4 | 290 | 2 | T24586 hypothetical prote |
| 39 | 109.5 | 8.4 | 330 | 2 | S4657 collagen alpha 1(X) |
| 40 | 109.5 | 8.4 | 488 | 2 | A27353 collagen alpha 1(I) |
| 41 | 109 | 8.4 | 1414 | 1 | S23809 collagen alpha 2(I) |
| 42 | 109 | 8.4 | 1418 | 2 | T45467 collagen alpha 1(I) |
| 43 | 109 | 8.4 | 1669 | 1 | CGMS4B collagen alpha 1(I) |
| 44 | 109 | 8.4 | 1744 | 2 | SA0991 collagen alpha 1(I) |
| 45 | 108.5 | 8.3 | 323 | 2 | A61396 collagen alpha 1(I) |

ALIGNMENTS

RESULT 1

S29328 complement subcomponent C1q chain C - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S29328

R/Petty, F., Reid, K.B.M., Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A/Title: Isolation, sequence analysis and characterization of cDNA clones coding for the ecercebellin.

A/Reference number: S29328; MUID:93011118; PMID:1396691

A/Accession: S29328

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-246 <PEP>

A/Cross-references: UNIPROT:002105; EMBL:X66295; NID:G50228; PIDN:CAA46993.1; PID:G50229

C/Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal homc F;122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 9.4%; Score 122.5; DB 2; Length 246;

Best Local Similarity 37.4%; Pred. No. 0.0015;

Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;

| | | |
|----|----|---|
| QY | 5 | GPASPRRLRLLLLLQLPAPSSASERPKKQKQRLRQREVLDLNGMCGPAGVPG 64 |
| DB | 4 | GPSCPQCGLCILLFLPLLRSQAS-----AGCYGIPGMPGAPG 47 |
| QY | 65 | RDGS--PGANVTPGTPGIGRDFKGEKGE 92 |
| DB | 48 | KDGHDLQSPKGEFGIPAVFGTQKPKQKGE 78 |

RESULT 2

A45407 collagen alpha 3 (IV) chain - sea urchin (Strongylocentrotus purpuratus)

C/Species: Strongylocentrotus purpuratus (purple urchin)

C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A45407; A43903; A23940

R/Exposito, J.Y., D'Alessio, M., Di Liberto, M., Ramirez, F.

J. Biol. Chem. 268, 5249-5254, 1993

A/Title: Complete primary structure of a sea urchin type IV collagen alpha chain and ana

A/Reference number: A45407; MUID:93186882; PMID:8444899

A/Accession: A45407

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-1752 <EXP>

A/Cross-references: UNIPROT:026312

A/Note: sequence extracted from NCBI backbone (NCBIP:126841)

R/Wessel, G.W., Etkin, M., Benson, S.

Dev. Biol. 148, 261-272, 1991

A/Title: Primary mesenchyme cells of the sea urchin embryo require an autonomously produc

A/Reference number: A43903; MUID:92038439; PMID:1936564

EMBO J. 8, 1705-1710, 1989
 A>Title: A base substitution in the exon of a collagen gene causes alternative splicing
 A:Reference number: S09400; MUID:89356643; PMID:2167050
 A:Accession: S09400
 A:Molecule type: mRNA
 A:Residues: 156-183 <ME1>
 R:Click, E.M.; Bornstein, P.
 Biochemistry 9, 4699-4706, 1970
 A>Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1
 A:Reference number: A90567; MUID:71038625; PMID:5529814
 A:Accession: CNBR0-1, CNBR2, CNBR4, CNBR5
 A:Molecule type: protein
 A:Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'B', 233, 'Z'
 A:Note: evidence for 170-alanine
 A:Experimental source: skin
 R:Baerige, B.; Noltbold, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, F.
 Eur. J. Biochem. 192, 153-159, 1990
 A>Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle
 A:Reference number: S11372; MUID:90382436; PMID:2169412
 A:Accession: S11372
 A:Molecule type: protein
 A:Residues: 175-187, 274-287, 'P', 289 <BA>
 A:Note: sequence of collagen alpha 1(S) (I) isolated from bone after pepsin digestion
 R:Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Manzi, S.A.; Gonzalez
 J. Biol. Chem. 266, 21827-21832, 1991
 A>Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
 A:Reference number: I55342; MUID:92042092; PMID:1718984
 A:Accession: I55342
 A:Molecule type: mRNA
 A:Residues: 258-268, 1347-1357 <DE>
 A:Cross-references: GB:S67495; NID:G239007; PIDN:AA20350.1; PID:G239008
 A:Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
 J. Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
 J. Biol. Chem. 245, 5042-5048, 1970
 A>Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
 A:Reference number: A92069; MUID:71001508; PMID:4319110
 A:Accession: A92069
 A:Molecule type: protein
 A:Residues: 263-268 <MOR>
 A:Experimental source: skin
 R:Labhard, M.E.; Hollister, D.W.
 Matrix 10, 124-130, 1990
 A>Title: Segmental amplification of the entire helical and telopeptide regions of the CD
 A:Reference number: S15989; MUID:90326017; PMID:2374517
 A:Accession: S15989
 A:Molecule type: mRNA
 A:Residues: 281-302, 402-420, 823-843, 925-944, 1026-1045, 1143-1162 <LAB>
 R:Wirt, M.K.; Rao, V.H.; Glaville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.
 Connect. Tissue Res. 29, 1-11, 1993
 A>Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
 A:Reference number: I52905; MUID:93339042; PMID:8339541
 A:Accession: I52905
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 342-352, 'C', 354-359 <MI2>
 A:Cross-references: GB:S64717; NID:G408195; PIDN:AA27677.1; PID:G408196
 A:Note: mutant sequence from patient with osteogenesis imperfecta
 R:Bernard, M.P.; Chu, M.L.; Weyer, J.C.; Ramirez, F.; Ekenberry, E.F.; Prockop, D.J.
 Biochemistry 22, 5213-5223, 1983
 A>Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1
 A:Reference number: A90476; MUID:84080385; PMID:6689127
 A:Accession: A90476
 A:Molecule type: mRNA
 A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464

 A:Cross-references: GB:K01228; NID:G180391; PIDN:AA45199.1; PID:G180392
 A:Note: sequence partially completed for missing nucleotides by A29439
 R:Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
 J. Biol. Chem. 260, 691-694, 1985
 A>Title: Multexon deletion in an osteogenesis imperfecta variant with increased type I

A:Reference number: A22161; MUID:85104934; PMID:2981843
 A:Accession: A22161
 A:Molecule type: DNA
 A:Residues: 472-594, 'R', 596-607 <CH3>
 A:Cross-references: GB:K03178; GB:K03179; NID:G179612; NID:G179613; PIDN:AA451847.1; PID:
 A:Note: the authors translated the codon CGT for residue 595 as Pro
 R:Wallis, G.A.; Starman, B.J.; Zimm, A.B.; Byers, P.H.
 Am. J. Hum. Genet. 46, 1034-1040, 1990
 A>Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
 A:Reference number: A35336; MUID:90252792; PMID:2339700
 A:Accession: A35336
 A:Molecule type: mRNA
 A:Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
 A:Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
 R:Forlino, A.; Zolazzi, F.; Valli, M.; Pignatelli, P.F.; Cetca, G.; Brunelli, P.C.; Mottes,
 Hum. Mol. Genet. 3, 2201-2206, 1994
 A>Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce
 A:Reference number: I54365; MUID:95187161; PMID:7881420
 A:Accession: I54365
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 746-766, 'S', 768-781 <FOR>
 A:Cross-references: GB:I47667; NID:G1009093; PIDN:AA59576.1; PID:G1009094
 R:Chesler, S.D.; Wallis, G.A.; Byers, P.H.
 J. Biol. Chem. 268, 18218-18225, 1993
 A>Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
 A:Reference number: A47426; MUID:93352646; PMID:8346997
 A:Accession: A47426
 A:Molecule type: mRNA
 A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>
 A:Cross-references: GB:S64596; NID:G407589; PIDN:AA27856.1; PID:G407590
 A:Note: sequence extracted from NCB1 backbone (NCBIN:136444, NCBI:136445)
 A:Note: does not represent an experimentally determined sequence but three different mut
 A:Accession: B47426
 A:Molecule type: mRNA
 A:Residues: 1179-1464 <CH4>
 A:Experimental source: normal dermal fibroblast culture
 A:Accession: C47426
 A:Molecule type: mRNA
 A:Residues: 1179-1276, 'H', 1278-1464 <CH5>
 A:Experimental source: fetal cell 86-237
 A:Accession: D47426
 A:Molecule type: mRNA
 A:Residues: 1179-1336, 1339-1464 <CH6>
 A:Experimental source: fetal cell 86-146
 A:Accession: E47426
 A:Molecule type: mRNA
 A:Residues: 1179-1387, 'R', 1389-1464 <CH7>
 A:Experimental source: fetal cell 88-251
 R:Conn, D.H.; Apone, S.; Byre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nick
 J. Biol. Chem. 263, 14605-14607, 1988
 A>Title: Substitution of Cysteine for glycine within the Carboxyl-terminal Telopeptide of
 A:Reference number: I55269; MUID:89008319; PMID:3170557
 A:Accession: I55269
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1187-1194, 'C', 1196-1220 <COH>
 A:Cross-references: GB:M23213; NID:G340842; PIDN:AA59363.1; PID:G499622
 A:Note: mutant sequence from a patient with mild osteogenesis imperfecta
 R:Maekela, J.K.; Raasina, M.; Vitra, A.; Vuorio, E.
 Nucleic Acids Res. 16, 349, 1988
 A>Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
 Query Match 9.1%; Score 118.5; DB 1; Length 1464;
 Best Local Similarity 36.3%; Pred. No. 0.027;
 Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;
 QY 3 PGGPAA--PQRLGILLULLLQLPAPSSASIPKQKQARQREVDVLYGMCLGPA 60
 DB 357 PGGPAA--PQRLGILLULLLQLPAPSSASIPKQKQARQREVDVLYGMCLGPA 60
 QY 61 GVGGRDGPAAVYIPGTGIPGRDGFKEGK 91

Db 386 GNPAGADGQPGKANGANGARIGADAPGPPARG 416

RESULT 5

T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29031
R/Mu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A/Description: The sequence of C. elegans cosmid F53G12.
A/Reference number: 220555
A/Accession: T29031
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-327 <MUX>
A/Cross-references: UNIPROT:O01799; EMBL:AF003139; PIDN:AAB54156.1; GSPDB:GN00019; CESP:
A/Experimental source: strain Bristol N2; clone F53G12
C/Genetics:
A/Gene: CESP:F53G12.7
A/Map position: 1
A/Introns: 59/3; 138/1; 223/2

Query Match
Best Local Similarity 9.0%; Score 117; DB 2; Length 327;
Matches 31; Conservative 2; Mismatches 22; Indels 38; Gaps 3;

QY 1 MRPGAPASPRRLGILLILLQLPAPSSASEIPKQKQKQLRQREVDLYNGMCLQGPA 60
Db 261 MGPGP-----PGPPG---PRGDKA-----GGHK 282
QY 61 GVPGRDGSPGANVPGTPGIPGRDGFGEKGEK 93
Db 283 GAPGDGPPGPGYKPGQPGAPGPDGSAKEKGC 315

RESULT 6

A55267
collagen alpha 5(IV) chain - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55267
R/Zheng, K.; Thorner, P.S.; Marrano, P.; Baumal, R.; McInnes, R.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 3989-3993, 1994
A/Title: Canine X chromosome-linked hereditary nephritis: a genetic model for human X-1
en type IV.
A/Reference number: A55267; MUID:94224868; PMID:8171024
A/Accession: A55267
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-754 <ZHS>
A/Cross-references: UNIPROT:Q28247; GB:U07888; NID:9469547; PIDN:AAB60258.1; PID:9469546
C/Superfamily: collagen alpha 1(IV) chain

Query Match
Best Local Similarity 9.0%; Score 117; DB 2; Length 754;
Matches 33; Conservative 7; Mismatches 34; Indels 22; Gaps 4;

QY 3 PPGAPASPRRLGILLILLQLPAPSSASEIP-----KGKO--KAQLRQREVDLYNGMCL 55
Db 332 PPGPPGR-----GLPGEGRGRLPGNGIKIGENGNCGQPGQPLPLKGD-- 377
QY 56 LQGPAGVGRDGSQGANVPGTPGIPGRDGFGEKGEK 91
Db 378 -QGPPIQGNRPGILNGMKDPLPGVPSPGPKMG 412

RESULT 7
S28791
collagen alpha 1(XI) chain - chicken (fragment)
C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S28791
R/Nah, H.D.; Barenbaum, M.; Upholt, W.B.

J. Biol. Chem. 267, 22581-22586, 1992
A/Title: The chicken alpha 1(XI) collagen gene is widely expressed in embryonic tissues.
A/Reference number: S28791; MUID:93054557; PMID:1429607
A/Accession: S28791
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-888 <NAH>

A/Cross-references: UNIPROT:Q90796; EMBL:M88593; NID:9211619; PIDN:AAA48707.1; PID:92116
C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
F:665-887/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match
Best Local Similarity 8.9%; Score 116; DB 2; Length 888;
Matches 31; Conservative 4; Mismatches 20; Indels 36; Gaps 3;

QY 3 PPGAPASPRRLGILLILLQLPAPSSASEIPKQKQKQLRQREVDLYNGMCLQGPA 60
Db 479 PPGAPGKPPGRLGIL-----PGVGE-----QGLP 504
QY 61 GVPGRDGSPGANVPGTPGIPGRDGFGEKGEK 91
Db 505 GAPGDGPPGPGYKPGQPGAPGPDGSAKEKGC 535

RESULT 8

CGHJ3B
collagen alpha 3(IV) chain precursor, long splice form - human
N/Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice form
C/Species: Homo sapiens (man)
C/Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A54763; A43928; A44043; A45971; A39786
R/Mariyama, M.; Leinonen, A.; Mochizuki, T.; Trygsvaen, K.; Reeders, S.T.
J. Biol. Chem. 269, 23013-23017, 1994
A/Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpression
A/Reference number: A54763; MUID:94364994; PMID:8083201
A/Accession: A54763
A/Molecule type: mRNA
A/Residues: 1-1670 <MAR>

A/Cross-references: UNIPROT:Q01955; GB:X80031; NID:9577563; PID:9577564
R/Experimental source: Kidney
R/Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Reese, A.; Pusey, C.D.
J. Clin. Invest. 89, 592-601, 1992
A/Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the alpha
A/Reference number: A43928; MUID:92147878; PMID:1737849
A/Accession: A43928
A/Molecule type: mRNA

A/Residues: 1331-1524, 'I', 1526-1670 <TUR>
A/Cross-references: GB:M81379
R/Experimental source: Kidney
R/Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 267, 19780-19784, 1992
A/Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpasture
A/Reference number: A44043; MUID:93015826; PMID:1400291
A/Accession: A44043
A/Molecule type: DNA; mRNA

A/Residues: 1386-1670 <QUT>
A/Cross-references: GB:M92993; NID:9177895; PIDN:AAA21610.1; PID:9177896
R/Note: sequence extracted from NCBI backbone (NCBI:P:115597)
R/Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A/Reference number: A44738; MUID:94274734; PMID:8006044
A/Contents: annotation; extracut; correction to intronic sequence in A44043
R/Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993

A/Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.
A/Reference number: A45971; MUID:93280184; PMID:8505332
A/Accession: A45971
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA

A:Residues: 1427-1444 <BER>
A>Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident
R.Morrison, K.E.; Maruyama, M.; Yang-Peng, T.L.; Reedere, S.T.
Am. J. Hum. Genet. 49, 545-554, 1991
A:Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of
A:Reference number: A39786; MUID:91353570; PMID:1882840
A:Accession: A39786
A:Molecule type: mRNA
A:Residues: 1453-1593 'A', 1595-1670 <MOR>
A:Cross-references: GB:S55790; NID:8234418; PIDN:AA19637.1; PID:8234419
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Comment: In Goodpasture's syndrome, an autoimmune response develops against an epitope
C:Function:
A:Gene: GDB:COL4A3
A:Cross-references: GDB:128351; OMIM:120070
A:Map position: 2q36-2q37
A:Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
A>Note: the alpha 3 (IV) and alpha 4 (IV) chain genes are encoded on opposite strands with
C:Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 3
among trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric
er associations in the interrupted helical domain (with disulfide and desmosine cross-
C:Function:
A:Description: minor structural component of extracellular basement membrane in kidney
C:Superfamily: collagen alpha 1 (IV) chain
C:Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extracel
F:1-28/Domain: signal sequence #status predicted <SIG>
F:129-1670/Product: collagen alpha 3 (IV) chain, long splice form #status predicted <MAT>
F:129-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F:143-1438/Region: interrupted helical
F:1791-793/Region: cell attachment (R-G-D) motif
F:1996-998/Region: cell attachment (R-G-D) motif
F:1154-1156/Region: cell attachment (R-G-D) motif
F:11306-1308/Region: cell attachment (R-G-D) motif
F:11345-1347/Region: cell attachment (R-G-D) motif
F:1432-1434/Region: cell attachment (R-G-D) motif
F:1433-1670/Domain: carboxyl-terminal nonhelical, NCI <NCI>
F:1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F:1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:131,33,39,41,125,422,476,479,682,722,809,1387/Disulfide bonds: interchain #status predi
F:253/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:1460-1548,1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F:1505-1511,1616-1622/Disulfide bonds: #status predicted
F:1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted

Query Match 8.9%; Score 116; DB 1; Length 1670;
Best Local Similarity 35.1%; Pred. No. 0.052;
Matches 33; Conservative 6; Mismatches 37; Indels 18; Gaps 3;

QY 5 GPASQGRRLGILLLLLPASSASERPKGQKQALQREVVVDLYNGMCICGPGVPG 64
Db 467 GPGGP-----GLCTCCPYIPGPPGAPGLHGVKGIPIR-----QGAAGLKG 511
QY 65 RDGSPGANVYPTGTGIRGD---GFGKGECELR 95
Db 512 SPGSPGNTGLPGRPFPGAGCGDGLKGEKGTITQ 545

RESULT 9
CGHU4B
collagen alpha 1 (IV) chain precursor - human
N:Alternate names: procollagen alpha 1 (IV) chain
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #sequence, revision 31-Dec-1992 #text, change 09-Jul-2004
C:Accession: S16876; A21117; S02738; S00048; S25826; A23115; S00207; S39614; A02863; A58
R:Solihnen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Trygvaason, K.
J. Biol. Chem. 264, 13565-13571, 1989
A:Title: Structural organization of the gene for the alpha-1 chain of human type IV coll
A:Reference number: S16876; MUID:89340433; PMID:2701944
A:Accession: S16876
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1669 <SO1>

A:Cross-references: UNIPROT:P02462; EMBL:J04217; GB:J05039; NID:9180800; PIDN:AA53098.1;
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1988
R.Solihnen, R.; Huotari, M.; Hoatlika, S.L.; Prockop, D.J.; Trygvaason, K.
J. Biol. Chem. 263, 17217-17220, 1988
A:Title: The structural genes for alpha1 and alpha2 chains of human type IV collagen are
A:Reference number: A92690; MUID:89034231; PMID:3182844
A:Accession: A32117
A:Molecule type: DNA
A:Residues: 1-28 <SO12>
A:Cross-references: EMBL:J04217; NID:9180759; PIDN:AA53097.1; PID:9553233
R:Poeshn, E.; Pollner, R.; Kuehn, K.
EMBO J. 7, 2687-2695, 1988
A:Title: The genes for the alpha1 (IV) and alpha2 (IV) chains of human basement membrane
A:Reference number: S02738; MUID:89030632; PMID:2846280
A:Accession: S02738
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6, 'L', '8-28 <PO>
A:Cross-references: EMBL:X12784; NID:930072
R:Brazel, D.; Oberhauser, I.; Dieringer, H.; Babel, W.; Glanville, R.W.; Deutzmann, R.;
Eur. J. Biochem. 168, 529-536, 1987
A:Title: Completion of the amino acid sequence of the alpha1 chain of human basement mem
A:Reference number: S00048; MUID:88029471; PMID:3311751
A:Accession: S00048
A:Molecule type: mRNA
A:Residues: 1-318, 'A', 320-944 <BRA1>
A:Cross-references: EMBL:X05561; NID:930066; PIDN:CAA29075.1; PID:930067
A:Accession: S25826
A:Molecule type: protein
A:Residues: 271-318, 'A', 320-554 <BRA2>
R:Glanville, R.W.; Qian, R.Q.; Siebold, B.; Risteli, J.; Kuehn, K.
Eur. J. Biochem. 152, 213-219, 1985
A:Title: Amino acid sequence of the N-terminal aggregation and cross-linking region (7S
A:Reference number: A23115; MUID:86004708; PMID:4043082
A:Accession: A23115
A:Molecule type: protein
A:Residues: 28-236, 'KE', 239-240, 'K', 242-243 <GLA>
A:Experimental source: placenta
A>Note: the amino end of the mature form is blocked
R:Solihnen, R.; Haka-Ristku, T.; Prockop, D.J.; Trygvaason, K.
FEBS Lett. 225, 188-194, 1987
A:Title: Complete primary structure of the alpha(1)-chain of human basement membrane (ty
A:Reference number: S00207; MUID:88083584; PMID:3691802
A:Accession: S00207
A:Molecule type: mRNA
A:Residues: 244-530 <SO13>
A:Cross-references: EMBL:Y00706; NID:929548; PIDN:CAA68698.1; PID:929549
R:Edle, J.A.; Golblak, R.; Mann, K.; Kuehn, K.
EMBO J. 12, 4795-4802, 1993
A:Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collagen n
A:Reference number: S39614; MUID:94038963; PMID:8223488
A:Accession: S39614
A:Molecule type: protein
A:Residues: 371-554 <EBL>
R:Babel, W.; Glanville, R.W.
Eur. J. Biochem. 143, 545-556, 1984
A:Title: Structure of human basement-membrane (type IV) collagen. Complete amino-acid seq
A:Reference number: A02863; MUID:85003629; PMID:6434307
A:Accession: A02863
A:Molecule type: protein
A:Residues: 534-718, 'D', 720-936, 'Y', 838-841, 'P', 843-903, 'Q', 905-913, 'K', 915-997, 'K', 999-1
A:Experimental source: placenta
R:Glanville, R.W.; Rauter, A.
Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A:Title: Peptide fragments of human placental basement-membrane collagens showing interrupt
A:Reference number: S16908; MUID:82005835; PMID:6792033
A:Accession: A58517
A:Molecule type: protein
A:Residues: 534-537, 'G', 539, 'G', 541-542, 'X', 544-553, 1389-1405, 'XX', 1408-1409, 'X', 1411-141
R:MacWhigty, R.S.; Benson, V.A.; Lovellio, K.T.; van der Rest, M.; Fietzek, F.P.
Biochemistry 22, 4940-4948, 1983
A:Title: Isolation and characterization of pepsin-solubilized human basement membrane (ty
A:Reference number: S16910; MUID:84053346; PMID:6416291

Biochemistry 16, 1158-1164, 1977
A>Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A/Reference number: A90399, PMID:77134724; PMID:557335
A/Accession: A90399
A/Molecule type: protein
A/Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEXY>
A/Experimental source: liver
A/Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R/Seyer, J.M.
submitted to the Atlas, December 1977
A/Reference number: A94562
A/Accession: A94562
A/Molecule type: protein
A/Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEXY>
A/Experimental source: liver
A/Note: author submitted corrections to A90399
R/Wilwicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldestein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A>Title: Parental somatic and germ-line mosaicism for a multilexon deletion with unusual
feeping.
A/Reference number: 151868; PMID:93304430; PMID:8317500
A/Accession: 151868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 186-194 <MTL>
A/Cross-references: GB:S62925; NID:9386425; PIDN:AAJ3937.1; PID:g4261637
R/Chido, A.A.; Silience, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A>Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A/Reference number: S59511; PMID:96067614; PMID:7487954
A/Accession: S59511
A/Molecule type: mRNA
A/Residues: 302-423 <CHI>
A/Cross-references: GB:S79877; NID:g1195576; PIDN:AA35615.1; PID:g1195577
R/Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
A>Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBR pe
A/Reference number: A90414; PMID:79000343; PMID:687591
A/Accession: A90414
A/Molecule type: protein
A/Residues: 399-675, 'N', 677-727 <SEXY>
A/Experimental source: liver
R/See, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A>Title: G to T transversion at position +5 of a splice donor site causes skipping of th
A/Reference number: 155349; PMID:91161621; PMID:1672129
A/Accession: 155349
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 537-605 <LEB>
A/Cross-references: GB:M59112; NID:g180815; PIDN:AA52041.1; PID:g180816
R/Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty
A/Reference number: A90438; PMID:80198282; PMID:6246925
A/Accession: A90438
A/Molecule type: protein
A/Residues: 728-895, 'A', 897-964 <SEXY>
A/Experimental source: liver
R/Cole, W.G.; Chido, A.A.; Lemande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Char
J. Biol. Chem. 265, 17070-17077, 1990
A>Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping an
A/Reference number: A38303; PMID:91009133; PMID:2145268
A/Accession: A38303
A/Molecule type: mRNA
A/Residues: 861-1015 <COL>
A/Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AA59383.1; PID:g
A/Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn
R/Manco, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A>Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
A/Reference number: S02119; PMID:88189827; PMID:3357782
A/Accession: S02119

A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
A/Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R/Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
A/Reference number: A90446; PMID:81208139; PMID:7016180
A/Accession: A90446
A/Molecule type: protein
A/Residues: 965-979, 'A', 981-984, 'PS', 987, 'ON', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-1
A/Experimental source: liver
R/oidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myer
Nucleic Acids Res. 12, 9383-9394, 1984
A>Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollagen
A/Reference number: A93551; PMID:85087944; PMID:6096827
A/Accession: A93551
A/Molecule type: mRNA
A/Residues: 1065-1155, 'P', 1157-1466 <LOI>
A/Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
R/Wiskuln, M.; Dalgleish, R.; Kluge-Beckerman, B.; Renard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1408-1413, 1986
A>Title: Human type III collagen gene expression is coordinately modulated with the type
A/Reference number: 152393; PMID:86187804; PMID:3754462
A/Accession: 152393
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1161-1200 <MS>
A/Cross-references: GB:M13146; NID:g180415; PIDN:AA52003.1; PID:g180416
R/Emanuel, B.S.; Camizazaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A>Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A/Reference number: 159025; PMID:85216505; PMID:3858826
A/Accession: 179339
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1165-1196 <EMA>
A/Cross-references: GB:M1134; NID:g180417; PIDN:AA52004.1; PID:g180418
R/Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Stippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha(III) collagen. P
A/Reference number: A92516; PMID:85157600; PMID:2579949
A/Accession: A92516
A/Molecule type: DNA
A/Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>
A/Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB:
A/Experimental source: liver
A/Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
action
C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O-
C/glycosylated.
A/Status: GDB:COL3A1
A/Cross-references: GDB:118729; OMIM:120180
A/Map position: 2q31-2q31
A/Introns: 27/1, 94/3, 111/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
A/Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
C/Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bo
er of their length, is formed with desmosine cross-links made from lysine and allylsine re
A/Function:
A/Description: structural component of extracellular fibrous polymer that maintains integ
C/Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C/Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-153/Domain: amino-terminal propeptide #status predicted <PRO>
F/1-91/Domain: von Willebrand factor type C repeat homology <VWC>
F/154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
F/154-167/Region: amino-terminal nonhelical telopeptide
F/168-1196/Region: helical
F/1091-1093/Region: cell attachment (R-G-D) motif
F/1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F/122-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F/1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

C/Accession: T26184
 R/Gardner, A.
 Submitted to the EMBL Data Library, October 1996
 A/Reference number: Z20166
 A/Accession: T26184
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-304 <WIL>
 A/Cross-references: UNIPROT:Q9XNG3; EMBL:Z61138; PDB:CB03474.1; GSPDB:GN00021; CESP:W0
 C/Genetics:
 A/Experimental source: clone W05B2
 A/Accession: CESP:W05B2.6
 A/Map position: 3
 A/Introns: 27/3

Query Match 8.8%; Score 114; DB 2; Length 304;
 Best Local Similarity 31.9%; Pred. No. 0.011;
 Matches 29; Conservative 5; Mismatches 25; Indels 32; Gaps 2;

QY 3 PGGPASPGRRLRLGLLLLLQLPAPSSASRIKPKXKQKQALRGREVVVDLYNMGMLGGPAGV 62
 Db 227 PGGP-----PGPAGSGPAGPAGPAGPAG-----APGPKGP 254

QY 63 PGRDGPANVIFGTPGIPGRDGFKEGKGC 93
 Db 255 SGAPGPGADGNNGAPGCGGCGSGAGEKGC 285

RESULT 15
 S22917
 N/Collagen alpha 5(IV) chain precursor, renal splice form - human
 N/Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence, revision 27-Feb-1997 #ext change 09-Jul-2004
 C/Accession: S22917; A54365; A57079; A37122; A34850; S18850; I56971; I76598; A35
 R./Zhou, J.; Hert, J.M.; Leinonen, A.; Trygvaason, K.
 J. Biol. Chem. 267, 12475-12481, 1992
 A/Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and identi
 n Alport syndrome patient.
 A/Reference number: S22917; MUID:92316923; PMID:1352287
 A/Accession: S22917
 A/Molecule type: mRNA
 A/Residues: 1-967 <ZHO>
 A/Cross-references: UNIPROT:P29400; GB:M90464; NID:G180826; PDB:AAA52046.1; PID:G553234
 R./Zhou, J.; Leinonen, A.; Trygvaason, K.
 J. Biol. Chem. 269, 6608-6614, 1994
 A/Title: Structure of the human type IV collagen COL4A5 gene.
 A/Reference number: A54365; MUID:94165049; PMID:8120014
 A/Accession: A54365
 A/Molecule type: DNA
 A/Residues: 1-922 <ZHO>
 A/Cross-references: GB:U04470; NID:G463378; GB:U04520; NID:G463428; PDB:AA27816.1; PID
 R./Zhou, J.; Mochizuki, T.; Smeets, H.; Antignac, C.; Laurilla, P.; de Paep, A.; Trygvaas
 Science 261, 1167-1169, 1993
 A/Title: Deletion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited sm
 A/Reference number: A57079; MUID:93361972; PMID:8356449
 A/Accession: A57079
 A/Molecule type: DNA
 A/Residues: 1-27 <ZHO>
 A/Cross-references: NID:G587203; PDB:CAA85512.1; PID:G587204
 R./Pihlajant, T.; Pihlajant, E.R.; Meyer, J.C.
 J. Biol. Chem. 265, 13758-13766, 1990
 A/Title: Complete primary structure of the triple-helical region and the carboxyl-termin
 A/Reference number: A37122; MUID:90337990; PMID:2380186
 A/Accession: A37122
 A/Molecule type: mRNA
 A/Residues: 84-439, 'GS', 442-624, 'LAIO', 629-666, 'FR', 669-887, 'R', 889-1264, 1271-1691 <PIH>
 A/Cross-references: GB:U05558; EMBL:M58526; NID:G1314209
 A/Note: Submitted to the EMBL Data Library, February 1991
 A/Note: the authors translated the codon GGC for residue 115 as Val
 R./Renieri, A.; Serri, M.; Meyer, J.C.; Pihlajant, T.; Massella, L.; Rizzoni, G.; De Ma
 Hum. Mol. Genet. 1, 127-129, 1992

A/Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid in /
 A/Reference number: I54317; MUID:93244772; PMID:1363780
 A/Accession: I54317
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 313-324, 'E', 326-330 <REN>
 A/Cross-references: GB:S59334; NID:G299946; PDB:AA013909.1; PID:G4261609
 R./Hostikka, S.L.; Bddy, R.L.; Byers, M.G.; Hoeythvae, M.; Shows, T.B.; Trygvaason, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990
 A/Title: Identification of a distinct type IV collagen alpha chain with restricted kidney
 A/Reference number: A34850; MUID:90160375; PMID:1689491
 A/Accession: A34850
 A/Molecule type: mRNA
 A/Residues: 914-1264, 1271-1691 <HOS>
 A/Cross-references: EMBL:M31115; NID:G180824; PDB:AAA52045.1; PID:G180825
 R./Zhou, J.; Hostikka, S.L.; Chow, L.T.; Trygvaason, K.
 Genomics 9, 1-9, 1991
 A/Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene that
 A/Reference number: A37969; MUID:91169491; PMID:2004755
 A/Accession: S18850
 A/Molecule type: DNA
 A/Residues: 924-1264, 1271-1691 <ZHO>
 A/Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459; EMBL
 8; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:G177922; PDB:AAA51558.1; PID:
 R./Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Bergh, H.; Cassiman, J.J.; Me
 kidney Int. 44, 1316-1321, 1993
 A/Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a complex
 A/Reference number: I56971; MUID:94133540; PMID:8301933
 A/Accession: I56971
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1258-1276 <GUO1>
 A/Cross-references: GB:S69168; NID:G545095; PDB:AA06012.1; PID:G545096
 A/Note: Kidney splice form
 A/Accession: I76598
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1284-1291, 'TRPGVLAQIV' <GUO2>
 A/Cross-references: GB:S69169; NID:G545097; PDB:AA06013.1; PID:G545098
 A/Note: frameshift mutation in patient with Alport syndrome
 R./Myers, J.C.; Jones, T.A.; Pihlajant, E.R.; Kadiri, A.S.; Goddard, A.D.; Sheer, D.; So
 Am. J. Hum. Genet. 46, 1024-1033, 1990
 A/Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the regio
 A/Reference number: A35335; MUID:90252791; PMID:2339699
 A/Accession: A35335
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1448-1477 <MYE>
 R./Nakazato, H.; Hattori, S.; Ushijima, T.; Matsura, T.; Koitabashi, Y.; Takada, T.; Yost
 kidney Int. 46, 1307-1314, 1994
 A/Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in primordi
 A/Reference number: I56975; MUID:95156893; PMID:7853788
 A/Accession: I56975
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1595-1602 <NAX>
 A/Cross-references: GB:S79903; NID:G913882; PDB:AA03374.1; PID:G913883
 A/Note: premature termination mutation from a patient with Alport syndrome; one other mut
 R./Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Trygvaason, K.; i
 Genomics 17, 485-489, 1993
 A/Title: Identification of four novel mutations in the COL4A5 gene of patients with Alpo
 A/Reference number: I54188; MUID:94010948; PMID:8406498
 A/Accession: I54188
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1604-1607, 'VHDAYXC' <LEW>
 A/Cross-references: GB:S65767; NID:G425563; PDB:AA013967.1; PID:G4261667
 A/Note: frameshift mutation from a patient with Alport syndrome; five other mutations are
 C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
 ed and subsequently O-glycosylated.
 C/Genetics:
 A/Genes: GDB:COL4A5; ATS
 A/Cross-references: GDB:120596; OMIM:303630

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:12:05 ; Search time 23 Seconds
(without alignments)
700.664 Million cell updates/sec

Title: US-10-063-734-122
Perfect score: 1301
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Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/1aa/backfile01.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1301 | 100.0 | 278 | 4 US-09-834-759-515 | Sequence 515, App |
| 3 | 1294 | 99.5 | 243 | 4 US-09-692-081-4 | Sequence 4, Appl1 |
| 4 | 1291 | 99.2 | 243 | 4 US-09-489-847-205 | Sequence 205, App |
| 5 | 1216 | 93.5 | 245 | 4 US-09-692-081-2 | Sequence 2, Appl1 |
| 6 | 1216 | 93.5 | 277 | 4 US-09-692-081-5 | Sequence 5, Appl1 |
| 7 | 1100.5 | 84.6 | 276 | 4 US-09-205-258-958 | Sequence 958, App |
| 8 | 1053 | 80.9 | 197 | 4 US-09-834-759-516 | Sequence 516, App |
| 9 | 1053 | 80.9 | 232 | 4 US-09-834-759-517 | Sequence 517, App |
| 10 | 356 | 27.4 | 66 | 4 US-09-205-258-962 | Sequence 962, App |
| 11 | 296 | 22.8 | 52 | 4 US-09-205-258-961 | Sequence 961, App |
| 12 | 270 | 20.8 | 51 | 4 US-09-205-258-963 | Sequence 963, App |
| 13 | 248 | 19.1 | 46 | 4 US-09-834-759-518 | Sequence 518, App |
| 14 | 211.5 | 16.3 | 52 | 4 US-09-205-258-960 | Sequence 960, App |
| 15 | 196 | 15.1 | 93 | 4 US-09-489-847-240 | Sequence 240, App |
| 16 | 196 | 15.1 | 93 | 4 US-09-489-847-362 | Sequence 362, App |
| 17 | 141 | 10.8 | 26 | 4 US-09-834-759-519 | Sequence 519, App |
| 18 | 122.5 | 9.4 | 246 | 2 US-08-463-911-4 | Sequence 4, Appl1 |
| 19 | 118.5 | 9.1 | 1057 | 3 US-08-931-820-1 | Sequence 1, Appl1 |
| 20 | 118.5 | 9.1 | 1461 | 4 US-09-585-887-9 | Sequence 9, Appl1 |
| 21 | 118.5 | 9.1 | 1461 | 4 US-09-289-578-9 | Sequence 9, Appl1 |
| 22 | 118.5 | 9.1 | 1464 | 4 US-09-331-347C-21 | Sequence 21, Appl1 |
| 23 | 115.5 | 8.9 | 128 | 3 US-09-227-357-190 | Sequence 190, App |
| 24 | 115 | 8.8 | 623 | 3 US-09-029-348-3 | Sequence 3, Appl1 |
| 25 | 115 | 8.8 | 626 | 3 US-09-029-348-2 | Sequence 2, Appl1 |
| 26 | 113.5 | 8.7 | 1694 | 1 US-08-494-168-2 | Sequence 2, Appl1 |
| 27 | 112.5 | 8.6 | 492 | 4 US-08-468-996-12 | Sequence 12, Appl1 |

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|----|-------|-----|------|-----------------------|--------------------|
| 28 | 112 | 8.6 | 96 | 4 US-09-513-999C-4206 | Sequence 4206, Ap |
| 29 | 112 | 8.6 | 208 | 4 US-09-800-729-151 | Sequence 151, App |
| 30 | 111 | 8.5 | 245 | 4 US-09-552-225A-4 | Sequence 4, Appl1 |
| 31 | 111 | 8.5 | 245 | 4 US-09-552-204A-4 | Sequence 4, Appl1 |
| 32 | 110.5 | 8.5 | 510 | 3 US-09-219-849-47 | Sequence 47, Appl1 |
| 33 | 110.5 | 8.5 | 595 | 3 US-09-219-849-48 | Sequence 48, Appl1 |
| 34 | 110.5 | 8.5 | 595 | 3 US-09-219-849-50 | Sequence 50, Appl1 |
| 35 | 110.5 | 8.5 | 684 | 1 US-08-555-669-12 | Sequence 12, Appl1 |
| 36 | 110.5 | 8.5 | 684 | 1 US-09-073-663-12 | Sequence 12, Appl1 |
| 37 | 110.5 | 8.5 | 755 | 4 US-09-919-497-57 | Sequence 57, Appl1 |
| 38 | 110.5 | 8.5 | 822 | 3 US-09-219-849-49 | Sequence 49, Appl1 |
| 39 | 110 | 8.5 | 258 | 4 US-09-976-594-815 | Sequence 815, App |
| 40 | 110 | 8.5 | 1568 | 3 US-09-181-706-2 | Sequence 2, Appl1 |
| 41 | 110 | 8.5 | 1568 | 3 US-09-458-791-2 | Sequence 2, Appl1 |
| 42 | 110 | 8.5 | 1568 | 3 US-09-459-066-2 | Sequence 2, Appl1 |
| 43 | 110 | 8.5 | 1568 | 4 US-09-459-065-2 | Sequence 2, Appl1 |
| 44 | 110 | 8.5 | 1806 | 4 US-09-919-497-56 | Sequence 56, Appl1 |
| 45 | 108.5 | 8.3 | 234 | 4 US-09-895-674A-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-834-759-514
; Sequence 514, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Diang, Yugui
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Hatlock, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834, 759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-514

Query Match 100.0%; Score 1301; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 9e-128;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MRPGPASPQRRLGILLLLQLPAPSSASEIPKQKQARQRRREVLDLYNGMCLQSPA | 60 |
| DB | 1 | MKPGPASPQRRLGILLLLQLPAPSSASEIPKQKQARQRRREVLDLYNGMCLQSPA | 60 |
| QY | 61 | GVPRGSGAGAVIRTPGIRPGDGRKRGKGLAREFSESTPNYKQCSWSLNYGIDL | 120 |
| DB | 61 | GVPRGSGAGAVIRTPGIRPGDGRKRGKGLAREFSESTPNYKQCSWSLNYGIDL | 120 |
| QY | 121 | GKIAECTFKMSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSLPFEAIYYLDO | 180 |
| DB | 121 | GKIAECTFKMSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSLPFEAIYYLDO | 180 |
| QY | 181 | GSPENNSTINIRTSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRRIIEE | 240 |
| DB | 181 | GSPENNSTINIRTSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRRIIEE | 240 |
| QY | 241 | LPR 243 | |
| DB | 241 | LPR 243 | |

RESULT 2

US-09-834-759-515
 ; Sequence 515, Application US/09834759
 ; Patent No. 6680197
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepner, William T.
 ; APPLICANT: Henderson, Robert A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.470C9
 ; CURRENT APPLICATION NUMBER: US/09/834,759
 ; CURRENT FILING DATE: 2001-04-13
 ; NUMBER OF SEQ ID NOS: 547
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 515
 ; LENGTH: 278
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-834-759-515

Query Match 100.0%; Score 1301; DB 4; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.1e-127;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 60
 DB 36 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 95
 QY 61 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
 DB 96 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 155
 QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 180
 DB 156 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 215
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 240
 DB 216 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 275
 QY 241 LPK 243
 DB 276 LPK 278

RESULT 3

US-09-692-081-4
 ; Sequence 4, Application US/09692081
 ; Patent No. 6630325
 ; GENERAL INFORMATION:
 ; APPLICANT: LINDNER, Volhard
 ; APPLICANT: FRIESEL, Robert F.
 ; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
 ; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
 ; CURRENT APPLICATION NUMBER: US/09/692,081
 ; CURRENT FILING DATE: 2000-10-19
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-692-081-4

Query Match 99.5%; Score 1294; DB 4; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.9e-127;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 60
 DB 1 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 60
 QY 61 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
 DB 61 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 180
 DB 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 4

US-09-489-847-205
 ; Sequence 205, Application US/09489847
 ; Patent No. 6476195
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al
 ; TITLE OF INVENTION: 98 Human Secreted Proteins
 ; FILE REFERENCE: P2031P1
 ; CURRENT APPLICATION NUMBER: US/09/489,847
 ; CURRENT FILING DATE: 2000-01-24
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130
 ; EARLIER FILING DATE: 1999-07-29
 ; EARLIER APPLICATION NUMBER: 60/094,657
 ; EARLIER FILING DATE: 1998-07-30
 ; EARLIER APPLICATION NUMBER: 60/095,486
 ; EARLIER FILING DATE: 1998-08-05
 ; EARLIER APPLICATION NUMBER: 60/096,319
 ; EARLIER FILING DATE: 1998-08-12
 ; EARLIER APPLICATION NUMBER: 60/095,454
 ; EARLIER FILING DATE: 1998-08-06
 ; EARLIER APPLICATION NUMBER: 60/095,455
 ; EARLIER FILING DATE: 1998-08-06
 ; NUMBER OF SEQ ID NOS: 376
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 205
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-489-847-205

Query Match 99.2%; Score 1291; DB 4; Length 243;
 Best Local Similarity 99.2%; Pred. No. 1e-126;
 Matches 241; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 60
 DB 1 MRPOGPASPORLRGLLLLLQLPAPSSASEIPKQKQKQRLRREVVLDYNGMCLQGPA 60
 QY 61 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
 DB 61 GVPGRDSSPGANVIRPOTPGIPGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 180
 DB 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLPIEATIIYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPRGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243


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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 958
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-958
Query Match      84.6%; Score 1100.5; DB 4; Length 276;
Best Local Similarity 96.7%; Pred. No. 9.7e-107;
Matches 203; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
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QY 34 PKGKQKALOREVVDLYNGMCLQGPAGVPRGDSFGANVIGTPIGRDGFKEKQEC 93
DB 68 PRG-SKRIRKREVDLYNGMCLQGPAGVPRGDSFGANVIGTPIGRDGFKEKQEC 126
QY 94 LRFSEFESWTNYKQCSWSLNYGIDLGKIAECTTKRSNALSRLVFSGLRLKCRVAC 153
DB 127 LRFSEFESWTNYKQCSWSLNYGIDLGKIAECTTKRSNALSRLVFSGLRLKCRVAC 186
QY 154 CORVYFTNGAECGSPLEIAIITYLDQSPENNSTINIHRTSSVEGLCEGIGAGLVVAVI 213
DB 187 CORVYFTNGAECGSPLEIAIITYLDQSPENNSTINIHRTSSVEGLCEGIGAGLVVAVI 246
QY 214 WVGTCSDYPKGDASTGMNSVRIIIEELPK 243
DB 247 WVGTCSDYPKGDASTGMNSVRIIIEELPK 276
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RESULT 8
US-09-834-759-516
; Sequence 516, Application us/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
```

```

; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 516
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-516
Query Match      80.9%; Score 1053; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.6e-102;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRPGPASPQRRLGLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
QY 61 GVPGRDSPGANVIGTPIGRDGFKEKQECLEAFSEFESWTNYKQCSWSLNYGIDL 120
DB 61 GVPGRDSPGANVIGTPIGRDGFKEKQECLEAFSEFESWTNYKQCSWSLNYGIDL 120
QY 121 GKIAECTTKRSNALSRLVFSGLRLKCRNACCQRYFTNGAECGSPLEIAIITYLDQ 180
DB 121 GKIAECTTKRSNALSRLVFSGLRLKCRNACCQRYFTNGAECGSPLEIAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSV 197
DB 181 GSPENNSTINIHRTSSV 197
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RESULT 9
US-09-834-759-517
; Sequence 517, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 517
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-517
Query Match      80.9%; Score 1053; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 7e-102;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRPGPASPQRRLGLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
DB 36 MRPGPASPQRRLGLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 95
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QY 61 GVPGRDGSAGNAVITPCTPGIPGRDGFKGEKGECLRESFESWTPTYKQCSWSLNVGIDL 120
DB 96 GVPGRDGSAGNAVITPCTPGIPGRDGFKGEKGECLRESFESWTPTYKQCSWSLNVGIDL 155
QY 121 GKIACTPTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPIEAIYYLDQ 180
DB 156 GKIACTPTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPIEAIYYLDQ 215
QY 181 GSPENNSTINIRTSV 197
DB 216 GSPENNSTINIRTSV 232

RESULT 10
US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205, 258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048, 885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 373

EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070, 923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092, 921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094, 657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 962
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-962

Query Match 27.4%; Score 356; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 8.3e-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 FTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPIEAIYYLDQSPENMS 187
DB 1 FTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPIEAIYYLDQSPENMS 60
QY 188 TINIR 193
DB 61 TINIR 66

RESULT 11
US-09-205-258-961
; Sequence 961, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205, 258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048, 885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 896

EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,020
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,876
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,895
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,884
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,894
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,971
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,964
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,882
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,899
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,893
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,900
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,901
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,892
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,915
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,019
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,970
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,972
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,916
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,373
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,875
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,374
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,917
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,949
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,974
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,883
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,897
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,898
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,962
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,963
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,877
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,878
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/070,923
 EARLIER FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 60/092,921
 EARLIER FILING DATE: 1996-07-15
 EARLIER APPLICATION NUMBER: 60/094,657
 NUMBER OF SEQ ID NOS: 1237
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 961
 LENGTH: 52

TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-205-258-961
 Query Match 22.8%; Score 296; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23; Mismatches 0; Indels 0; Gaps 0;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cy 77 TPQIPGRDGFKEKGEKCEKRESFESEWTPTNYQCSWSSLNTGIDIGKTAECTF 128
 Db 1 TQPIRDSGFKEKGEKCEKRESFESEWTPTNYQCSWSSLNTGIDIGKTAECTF 52
 RESULT 12
 US-09-205-258-963
 Sequence 963, Application US/09205258
 Patent No. 6525174
 GENERAL INFORMATION:
 APPLICANT: Young et al.
 TITLE OF INVENTION: 207 Human Secreted Proteins
 FILE REFERENCE: P2007P1
 CURRENT APPLICATION NUMBER: US/09/205,258
 EARLIER FILING DATE: 1998-12-04
 EARLIER APPLICATION NUMBER: PCT/US98/11422
 EARLIER FILING DATE: 1998-06-04
 EARLIER APPLICATION NUMBER: 60/048,885
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,375
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,881
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,880
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,896
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,020
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,876
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,895
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,884
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,894
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,971
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,964
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,882
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,899
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,893
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,900
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,901
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,892
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,915
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,019
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,970
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,972
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,916
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,373
 EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 963
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-963

Query Match 20.8%; Score 270; DB 4; Length 51;
Best Local Similarity 100.0%; Pred.No. 5,6e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 RTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEELPK 243
Db 1 RTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEELPK 51

RESULT 13
US-09-834-759-518
Sequence 518, Application US/09834759
Patent No. 6660197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 518
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-759-518

Query Match 19.1%; Score 248; DB 4; Length 46;

Best Local Similarity 100.0%; Pred.No. 9.7e-19;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 EELCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEELPK 243
Db 1 EELCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEELPK 46

RESULT 14
US-09-205-258-960
Sequence 960, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
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EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-960

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Query Match
Best Local Similarity 16.3%; Score 211.5; DB 4; Length 52;
Matches 40; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 34 PKGKQAKLQREVRVLDLYNGMCLQGPAGVGRDSDPGANVTPGTPTGI 80
Db 7 PRG-SKRRIRQREVVDLYNGMCLQGPAGVGRDSDPGANVTPGTPTGI 52

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RESULT 15
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/117130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-240

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Query Match 15.1%; Score 196; DB 4; Length 93;

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Best Local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRPGPASPQRURGLLLILLQLPAPSSASIEIPKQKXA 40
Db 1 MRPGPASPQRURGLLLILLQLPAPSSASIEIPKQKXA 40

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Search completed: December 25, 2004, 05:28:28
Job time : 24 secs


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RESULT 2
US-09-834-759-515
; Sequence 515, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-515
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Query Match      100.0%; Score 243; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 2e-227;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 60
      36 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 95
DB
QY      61 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 120
      96 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
DB      121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 180
      156 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 215
QY      181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPKGDASTGMNSVSRITIEE 240
      216 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPKGDASTGMNSVSRITIEE 275
DB
QY      241 LPK 243
      |||
DB      276 LPK 278
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RESULT 3
US-09-834-759-516
; Sequence 516, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 516
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-834-759-516
Query Match      81.1%; Score 197; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 60
      36 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 95
DB
QY      61 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 120
      96 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
DB      121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 180
      156 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 215
QY      181 GSPENNSTINIHRTSSV 197
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DB      181 GSPENNSTINIHRTSSV 197
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RESULT 4
US-09-834-759-517
; Sequence 517, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 517
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-517
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Query Match      81.1%; Score 197; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.6e-183;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 60
      36 MRPOGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMCLOGPA 95
DB
QY      61 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 120
      96 GVGGRDGSFGANVITGTGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
DB      121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 180
      156 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLQ 215
QY      181 GSPENNSTINIHRTSSV 197
      |||
DB      216 GSPENNSTINIHRTSSV 232
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RESULT 5
US-09-692-081-4
; Sequence 4, Application US/09692081
; Patent No. 6610325
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; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: PRIESEL, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-692-081-4

Query Match      70.0%; Score 170; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGIPGRDGFKEKGEKCLRESFESWTPTNYKOCSSSLNYGIDLGKIACTFTKMS 133
DB 74 IPGTGIPGRDGFKEKGEKCLRESFESWTPTNYKOCSSSLNYGIDLGKIACTFTKMS 133
QY 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGACSGPLPIEAIITYDQSPENNSTINHR 193
DB 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGACSGPLPIEAIITYDQSPENNSTINHR 193
QY 194 TSSVEGLCEGIGAGLVDAIWMGTGSDYKGDASTGMSVSRITIEELPK 243
DB 194 TSSVEGLCEGIGAGLVDAIWMGTGSDYKGDASTGMSVSRITIEELPK 243

RESULT 6
US-09-205-258-958
; Sequence 958, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 958
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-205-258-958

Query Match      70.0%; Score 170; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGIPGRDGFKEKGEKCLRESFESWTPTNYKOCSSSLNYGIDLGKIACTFTKMS 133
DB 107 IPGTGIPGRDGFKEKGEKCLRESFESWTPTNYKOCSSSLNYGIDLGKIACTFTKMS 166
QY 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGACSGPLPIEAIITYDQSPENNSTINHR 193
DB 167 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGACSGPLPIEAIITYDQSPENNSTINHR 226
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QY 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPKPGDASTGMNSVSRITIELPK 243
DB 227 TSSVEGLCEGIGAGLVDAIWMGTCSDPKPGDASTGMNSVSRITIELPK 276

RESULT 7

US-09-692-081-2
; Sequence 2, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-692-081-2

Query Match
Best Local Similarity 45.7%; Score 111; DB 4; Length 245;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFGEKGECLRESFESWTPTYKQCSWSLNYGIDIGKIAECTFTKMS 133
DB 76 IPGTGPIGRDGFGEKGECLRESFESWTPTYKQCSWSLNYGIDIGKIAECTFTKMS 135
QY 134 NSALRVLFSSGLRLKCRNACCORWYFTFNAGCSGPIPIAIIYLDGSP 184
DB 136 NSALRVLFSSGLRLKCRNACCORWYFTFNAGCSGPIPIAIIYLDGSP 186

RESULT 8

US-09-692-081-5
; Sequence 5, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-692-081-5

Query Match
Best Local Similarity 45.7%; Score 111; DB 4; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFGEKGECLRESFESWTPTYKQCSWSLNYGIDIGKIAECTFTKMS 133
DB 108 IPGTGPIGRDGFGEKGECLRESFESWTPTYKQCSWSLNYGIDIGKIAECTFTKMS 167
QY 134 NSALRVLFSSGLRLKCRNACCORWYFTFNAGCSGPIPIAIIYLDGSP 184
DB 168 NSALRVLFSSGLRLKCRNACCORWYFTFNAGCSGPIPIAIIYLDGSP 218

RESULT 9

US-09-489-847-205
; Sequence 205, Application US/09489847
; Patent No. 6476195

GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-205

Query Match
Best Local Similarity 36.2%; Score 88; DB 4; Length 243;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 RMYFTFNAGCSGPIPIAIIYLDGSPENSTINIHRTSSVEGLCEGIGAGLVDAIWM 215
DB 156 RMYFTFNAGCSGPIPIAIIYLDGSPENSTINIHRTSSVEGLCEGIGAGLVDAIWM 215
QY 216 GTCSDPKPGDASTGMNSVSRITIELPK 243
DB 216 GTCSDPKPGDASTGMNSVSRITIELPK 243

RESULT 10

US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 962
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-962

Query Match 27.2%; Score 66; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2e-56;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 FTKMNSALRYLFGSSLLKCRNACCCWYFFFNAGSGSPPIRATIIYDDGSPBNMS 187
DB 1 FTKMNSALRYLFGSSLLKCRNACCCWYFFFNAGSGSPPIRATIIYDDGSPBNMS 60
QY 188 TINHR 193

Db 61 TINHR 66
RESULT 11
US-09-205-258-961
Sequence 961, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,971
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974

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| Matches | 51; | Conservative | 0; | Mismatches | 0; |
| | | | | Indels | 0; |
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| QY | 193 | RTSSVEGLCEGIGAGLVDAIWTGTCSDYKPGASTGNNVSRIITIEELPK | 243 | | |
| Db | 1 | RTSSVEGLCEGIGAGLVDAIWTGTCSDYKPGASTGNNVSRIITIEELPK | 51 | | |

US-09-834-759-518
; Sequence 518, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 518
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-518

Query Match 18.9%; Score 46; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 EGI CEGIGAGLVDAIWTGTCSDYPRGDASTGMSVSRIIIIEPLK 243
DB 1 EGI CEGIGAGLVDAIWTGTCSDYPRGDASTGMSVSRIIIIEPLK 46

RESULT 14
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-240

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.4e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQK 40
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQK 40

RESULT 15

US-09-489-847-362
; Sequence 362, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 362
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-362

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.4e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQK 40
DB 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQK 40

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-063-734-122

Perfect score: 243
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Searched: 1595201 seqs, 359116952 residues

Wordsize: 6

Total number of hits satisfying chosen parameters: 31080

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 243 | 100.0 | 243 | 9 | US-09-838-418-7 |
| 3 | 243 | 100.0 | 243 | 10 | US-09-946-374-352 |
| 4 | 243 | 100.0 | 243 | 10 | US-09-946-374-431 |
| 5 | 243 | 100.0 | 243 | 13 | US-10-006-867-122 |
| 6 | 243 | 100.0 | 243 | 13 | US-10-052-586-366 |
| 7 | 243 | 100.0 | 243 | 13 | US-10-007-805-514 |
| 8 | 243 | 100.0 | 243 | 13 | US-10-063-547-122 |
| 9 | 243 | 100.0 | 243 | 13 | US-10-063-551-122 |
| 10 | 243 | 100.0 | 243 | 14 | US-10-174-590-366 |
| 11 | 243 | 100.0 | 243 | 14 | US-10-176-758-366 |
| 12 | 243 | 100.0 | 243 | 14 | US-10-175-737-366 |
| 13 | 243 | 100.0 | 243 | 14 | US-10-063-616-122 |

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| 15 | 243 | 100.0 | 243 | 14 | US-10-176-483-366 | Sequence 366, App |
| 16 | 243 | 100.0 | 243 | 14 | US-10-176-749-366 | Sequence 366, App |
| 17 | 243 | 100.0 | 243 | 14 | US-10-176-914-366 | Sequence 366, App |
| 18 | 243 | 100.0 | 243 | 14 | US-10-176-915-366 | Sequence 366, App |
| 19 | 243 | 100.0 | 243 | 14 | US-10-063-569-122 | Sequence 122, App |
| 20 | 243 | 100.0 | 243 | 14 | US-10-063-513-122 | Sequence 122, App |
| 21 | 243 | 100.0 | 243 | 14 | US-10-063-515-122 | Sequence 122, App |
| 22 | 243 | 100.0 | 243 | 14 | US-10-063-512-122 | Sequence 122, App |
| 23 | 243 | 100.0 | 243 | 14 | US-10-173-706-366 | Sequence 366, App |
| 24 | 243 | 100.0 | 243 | 14 | US-10-175-738-366 | Sequence 366, App |
| 25 | 243 | 100.0 | 243 | 14 | US-10-175-752-366 | Sequence 366, App |
| 26 | 243 | 100.0 | 243 | 14 | US-10-176-482-366 | Sequence 366, App |
| 27 | 243 | 100.0 | 243 | 14 | US-10-176-757-366 | Sequence 366, App |
| 28 | 243 | 100.0 | 243 | 14 | US-10-176-913-366 | Sequence 366, App |
| 29 | 243 | 100.0 | 243 | 14 | US-10-180-552-366 | Sequence 366, App |
| 30 | 243 | 100.0 | 243 | 14 | US-10-180-557-366 | Sequence 366, App |
| 31 | 243 | 100.0 | 243 | 14 | US-10-076-622-514 | Sequence 514, App |
| 32 | 243 | 100.0 | 243 | 14 | US-10-063-502-122 | Sequence 122, App |
| 33 | 243 | 100.0 | 243 | 14 | US-10-173-700-366 | Sequence 366, App |
| 34 | 243 | 100.0 | 243 | 14 | US-10-174-572-366 | Sequence 366, App |
| 35 | 243 | 100.0 | 243 | 14 | US-10-174-579-366 | Sequence 366, App |
| 36 | 243 | 100.0 | 243 | 14 | US-10-174-582-366 | Sequence 366, App |
| 37 | 243 | 100.0 | 243 | 14 | US-10-174-588-366 | Sequence 366, App |
| 38 | 243 | 100.0 | 243 | 14 | US-10-175-739-366 | Sequence 366, App |
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| 40 | 243 | 100.0 | 243 | 14 | US-10-175-743-366 | Sequence 366, App |
| 41 | 243 | 100.0 | 243 | 14 | US-10-176-488-366 | Sequence 366, App |
| 42 | 243 | 100.0 | 243 | 14 | US-10-176-492-366 | Sequence 366, App |
| 43 | 243 | 100.0 | 243 | 14 | US-10-176-747-366 | Sequence 366, App |
| 44 | 243 | 100.0 | 243 | 14 | US-10-176-750-366 | Sequence 366, App |
| 45 | 243 | 100.0 | 243 | 14 | US-10-176-985-366 | Sequence 366, App |

ALIGNMENTS

RESULT 1
US-09-834-759-514
; Sequence 514, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jilong, Yugu
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-514
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Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFEESWTPTVYKQCSWSLNYGIDL 120

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Db 121 GKIACFTTKRNSALRVLPFGSLRLKCRNACCCORWYFTNGACSGPLPIEATYYDQ 180
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Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
Db 241 LPK 243

RESULT 2
US-09-938-418-7
; Sequence 7, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Polakis, Paul
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
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; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
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; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-938-418-7

Query Match 100.0%; Score 243; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 1,8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLLLLPAPSSASEIRPKQKQOLQREVVLDLYNMCQGRA 60
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QY 61 GVPGRDGSFGANVLPGTGIGRDPFGKEGCECLRESFEESWTPNYKQCSWSLNYGIDL 120
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QY 241 LPK 243
Db 241 LPK 243

RESULT 3
US-09-946-374-352
; Sequence 352, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PICI
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01

APPLICANT: Larey, Kevin F.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374

[illegible]

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;; PRIOR FILING DATE: 1998-09-18
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;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 243; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 1,8e-211; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

Qy 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGGKAKOLRORRVLDLNGMCLQGP 60
Db 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGGKAKOLRORRVLDLNGMCLQGP 60
Qy 61 GVPGRDSPGANVTPGTGIPGRDGFGEKGECLRESFESWTPNYKQCSWSLNYGIDL 120
Db 61 GVPGRDSPGANVTPGTGIPGRDGFGEKGECLRESFESWTPNYKQCSWSLNYGIDL 120
Qy 121 GKIAECTFTKMSNSALRYLFGSGLKCRNACCORWYTFNGAECSGFLPEAIYYLDO 180
Db 121 GKIAECTFTKMSNSALRYLFGSGLKCRNACCORWYTFNGAECSGFLPEAIYYLDO 180
Qy 181 GSPENSTINIRHTSVEGLCEGIGLVDAIHWGTGSDYPRGDASTGMSVRIIEE 240
Db 181 GSPENSTINIRHTSVEGLCEGIGLVDAIHWGTGSDYPRGDASTGMSVRIIEE 240
Qy 241 LPK 243
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RESULT 5
US-10-006-867-122
; Sequence 122, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gutney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; PRIOR APPLICATION NUMBER: 2001-12-06
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/064215
 PRIOR FILING DATE: 1997-10-29
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 PRIOR FILING DATE: 1998-04-22
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 PRIOR FILING DATE: 1999-01-22
 PRIOR APPLICATION NUMBER: 60/119285
 PRIOR FILING DATE: 1999-02-09

APPLICANT: Smith,Victoria
APPLICANT: Matanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
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1 PRIOR APPLICATION NUMBER: 60/079664
 2 PRIOR FILING DATE: 1998-03-27
 3 PRIOR APPLICATION NUMBER: 60/079786
 4 PRIOR FILING DATE: 1998-03-27
 5 PRIOR APPLICATION NUMBER: 60/080107
 6 PRIOR FILING DATE: 1998-03-31
 7 PRIOR APPLICATION NUMBER: 60/080194
 8 PRIOR FILING DATE: 1998-03-31
 9 PRIOR APPLICATION NUMBER: 60/080327
 10 PRIOR FILING DATE: 1998-04-01
 11 PRIOR APPLICATION NUMBER: 60/080333
 12 PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
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 PRIOR FILING DATE: 1998-04-09
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 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084639
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 PRIOR APPLICATION NUMBER: 60/084640
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 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
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 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 243; DB 13; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1,8e-211;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQALROREVVLDLYNMCLOGPA 60
 Db 1 MRPGPASPORLRLGILLILLQLPAPSSASEIPKQKQALROREVVLDLYNMCLOGPA 60
 QY 61 GVPGRGSPRANVTPTGPIRGDGFKEGEGCLRESEESWTPNYKQCSWSLNYGIDL 120
 Db 61 GVPGRGSPRANVTPTGPIRGDGFKEGEGCLRESEESWTPNYKQCSWSLNYGIDL 120
 QY 121 GKIAECTFTKMSNSALRYLFGSLRLKCRNACCORWFTNGAECGGLPIEAIITLDO 180
 Db 121 GKIAECTFTKMSNSALRYLFGSLRLKCRNACCORWFTNGAECGGLPIEAIITLDO 180
 QY 181 GSPBNMSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGNNVSRIITIE 240
 Db 181 GSPBNMSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGNNVSRIITIE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 7
 US-10-007-805-514
 ; Sequence 514, Application US/10007805


```
Publication No. US20020150581A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuguo
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hedler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margalita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C10
CURRENT APPLICATION NUMBER: US/10/007,805
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 514
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-805-514

Query Match      100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
DB 1 MRQGPAAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
QY 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
QY 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRIIIEE 240
DB 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 8
US-10-063-547-122
Sequence 122, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 122
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LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-547-122

Query Match      100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
DB 1 MRQGPAAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
QY 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
QY 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRIIIEE 240
DB 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243
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RESULT 9
US-10-063-551-122
Sequence 122, Application US/10063551
Publication No. US20020183494A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,551
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 122
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-551-122

Query Match      100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
DB 1 MRQGPAAASPORLRGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMCLOGPA 60
QY 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDGSFGANVITPTPGIPGRDGFKEGKEGCELRSEFESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
DB 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCORWYFTFGAECGSLPIEAIITYLDQ 180
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Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPAAPORLRLGLLLLLLLLPAPSSASEIPKQKQAOQLRQREVVDLYNMCLOGPA 60
DB 1 MRPOGPAAPORLRLGLLLLLLLLPAPSSASEIPKQKQAOQLRQREVVDLYNMCLOGPA 60
QY 61 GVPGRDPSGANVYIPETPGIPGRDGFKGKGECLRSFESWTPNYKQCSWSLNYGIDL 120
DB 61 GVPGRDPSGANVYIPETPGIPGRDGFKGKGECLRSFESWTPNYKQCSWSLNYGIDL 120
QY 121 GXIAECTFTKMSNSALRYLFGSGLRLKCRNACCQWYFTFNGACSGPLPIEAIITYLQ 180
DB 121 GXIAECTFTKMSNSALRYLFGSGLRLKCRNACCQWYFTFNGACSGPLPIEAIITYLQ 180
QY 181 GSPEMNSTINIRHTSSVEGLCEGIGALVDVAIWGTCSDYPKGDASTGMSVSRITIEE 240
DB 181 GSPEMNSTINIRHTSSVEGLCEGIGALVDVAIWGTCSDYPKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 13
US-10-063-616-122
; Sequence 122, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritson, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-122

Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPAAPORLRLGLLLLLLLLPAPSSASEIPKQKQAOQLRQREVVDLYNMCLOGPA 60
DB 1 MRPOGPAAPORLRLGLLLLLLLLPAPSSASEIPKQKQAOQLRQREVVDLYNMCLOGPA 60
QY 61 GVPGRDPSGANVYIPETPGIPGRDGFKGKGECLRSFESWTPNYKQCSWSLNYGIDL 120
DB 61 GVPGRDPSGANVYIPETPGIPGRDGFKGKGECLRSFESWTPNYKQCSWSLNYGIDL 120
QY 121 GXIAECTFTKMSNSALRYLFGSGLRLKCRNACCQWYFTFNGACSGPLPIEAIITYLQ 180
DB 121 GXIAECTFTKMSNSALRYLFGSGLRLKCRNACCQWYFTFNGACSGPLPIEAIITYLQ 180
QY 181 GSPEMNSTINIRHTSSVEGLCEGIGALVDVAIWGTCSDYPKGDASTGMSVSRITIEE 240
DB 181 GSPEMNSTINIRHTSSVEGLCEGIGALVDVAIWGTCSDYPKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

DB 241 LPK 243

RESULT 14
US-10-174-581-366
; Sequence 366, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174, 581
; CURRENT FILING DATE: 2002-06-18
; Prior Application Number: 10/052586
; Prior Filing Date: 2002-01-15
; Prior Application Number: 60/059263
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/059266
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/062250
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063120
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063121
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063486
; Prior Filing Date: 1997-10-21
; Prior Application Number: 60/063540
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063541
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; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063564
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; Prior Application Number: 60/063734
; Prior Filing Date: 1997-10-29
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; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/065311
; Prior Filing Date: 1997-11-13
; Prior Application Number: 60/066120
; Prior Filing Date: 1997-11-21
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; Prior Filing Date: 1997-11-24
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; Prior Filing Date: 1997-11-24
; Prior Application Number: 60/069335
; Prior Filing Date: 1997-12-11
; Prior Application Number: 60/069425
; Prior Filing Date: 1997-12-12
; Prior Application Number: 60/069870
; Prior Filing Date: 1997-12-17
; Prior Application Number: 60/068017
; Prior Filing Date: 1997-12-18
; Prior Application Number: 60/07450
; Prior Filing Date: 1998-03-10
; Prior Application Number: 60/077632
; Prior Filing Date: 1998-03-11

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 PRIOR FILING DATE: 1998-03-11
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 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
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 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
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 PRIOR APPLICATION NUMBER: 60/087208

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 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 243; DB 14; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1,8e-211;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRQGPASPORLRLRLLLLLQPPASSASEIPKQKQQLRQREVVDLYNGMCLQGP 60
 DB 1 MRQGPASPORLRLRLLLLLQPPASSASEIPKQKQQLRQREVVDLYNGMCLQGP 60
 QY 61 GVPGRDGSFGANVLPGRPGIPGRDGFKEGKECIRSFESFESWTNPKQCSWSLNGIDL 120
 DB 61 GVPGRDGSFGANVLPGRPGIPGRDGFKEGKECIRSFESFESWTNPKQCSWSLNGIDL 120

```
QY 121 GKIAECTFTKMRNSALRYLFGSGLRLKCRNACCCORWYFTFNGACSGPLPIEAIITYLDQ 180
    |||
DB 121 GKIAECTFTKMRNSALRYLFGSGLRLKCRNACCCORWYFTFNGACSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPRKGDASTGMNSYSRIIIEE 240
    |||
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPRKGDASTGMNSYSRIIIEE 240
QY 241 LPK 243
    |||
DB 241 LPK 243
```

RESULT 15

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US-10-176-483-366
; Sequence 366, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; PRIOR FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-366
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Query Match 100.0%; Score 243; DB 14; Length 243;

Best Local Similarity 100.0%; Pred. No. 1.8e-211; Mismatches 0; Indels 0; Gaps 0;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPOGPAASPORLGLLLLLQLPAPSSASEIPKSKOKAQLRQREVDLYNGMCLQGPA 60
    |||
DB 1 MRPOGPAASPORLGLLLLLQLPAPSSASEIPKSKOKAQLRQREVDLYNGMCLQGPA 60
QY 61 GYPGRDGSFGANYIPGTGPIGRDGFKEGKECLRESFESWTPNTKQCSWSSLYNGIDL 120
    |||
DB 61 GYPGRDGSFGANYIPGTGPIGRDGFKEGKECLRESFESWTPNTKQCSWSSLYNGIDL 120
QY 121 GKIAECTFTKMRNSALRYLFGSGLRLKCRNACCCORWYFTFNGACSGPLPIEAIITYLDQ 180
    |||
DB 121 GKIAECTFTKMRNSALRYLFGSGLRLKCRNACCCORWYFTFNGACSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPRKGDASTGMNSYSRIIIEE 240
    |||
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPRKGDASTGMNSYSRIIIEE 240
QY 241 LPK 243
    |||
DB 241 LPK 243
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Search completed: December 25, 2004, 05:35:09
Job time : 70 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 05:28:06 ; Search time 23 Seconds
(without alignments)
1016.551 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 243

Sequence: 1 MKPGCPAASPTLRGLL...GDASTGWNVSRIIEBLPK 243

Scoring table: <OLIGO>
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 6

Total number of hits satisfying chosen parameters: 1982

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 9 | 3.7 | 133 | 2 | S57038 |
| 2 | 9 | 3.7 | 144 | 2 | T18867 |
| 3 | 9 | 3.7 | 247 | 2 | A55717 |
| 4 | 9 | 3.7 | 779 | 1 | CG801S |
| 5 | 9 | 3.7 | 996 | 2 | JB0237 |
| 6 | 9 | 3.7 | 1464 | 1 | CGHUIS |
| 7 | 8 | 3.3 | 112 | 2 | AG0111 |
| 8 | 8 | 3.3 | 141 | 1 | UTRUB |
| 9 | 8 | 3.3 | 165 | 1 | KTHUB |
| 10 | 8 | 3.3 | 169 | 2 | T18321 |
| 11 | 8 | 3.3 | 177 | 2 | S37749 |
| 12 | 8 | 3.3 | 249 | 2 | T35724 |
| 13 | 8 | 3.3 | 254 | 2 | T38427 |
| 14 | 8 | 3.3 | 291 | 2 | B60131 |
| 15 | 8 | 3.3 | 296 | 2 | T24827 |
| 16 | 8 | 3.3 | 302 | 2 | T21257 |
| 17 | 8 | 3.3 | 307 | 2 | S36779 |
| 18 | 8 | 3.3 | 330 | 2 | S46657 |
| 19 | 8 | 3.3 | 333 | 2 | T20436 |
| 20 | 8 | 3.3 | 360 | 2 | T37285 |
| 21 | 8 | 3.3 | 365 | 2 | UC7694 |
| 22 | 8 | 3.3 | 368 | 2 | AE0086 |
| 23 | 8 | 3.3 | 378 | 2 | T00481 |
| 24 | 8 | 3.3 | 391 | 2 | D72663 |
| 25 | 8 | 3.3 | 399 | 2 | CB6611 |
| 26 | 8 | 3.3 | 424 | 2 | C70371 |
| 27 | 8 | 3.3 | 457 | 1 | RMGST4 |
| 28 | 8 | 3.3 | 487 | 1 | A26660 |
| 29 | 8 | 3.3 | 487 | 2 | S54785 |

| | | | | | | |
|----|---|-----|------|---|--------|---------------------|
| 30 | 8 | 3.3 | 500 | 2 | S66522 | cartilage matrix p |
| 31 | 8 | 3.3 | 636 | 2 | S41067 | collagen alpha 1(I) |
| 32 | 8 | 3.3 | 674 | 2 | S23297 | collagen alpha 1(X) |
| 33 | 8 | 3.3 | 809 | 2 | A45747 | Na+/H+-exchanging |
| 34 | 8 | 3.3 | 917 | 2 | S09646 | collagen alpha 2(V) |
| 35 | 8 | 3.3 | 984 | 2 | S67527 | protein kinase (EC |
| 36 | 8 | 3.3 | 1018 | 1 | CGH02A | collagen alpha 2(V) |
| 37 | 8 | 3.3 | 1029 | 1 | S21369 | collagen alpha 1(X) |
| 38 | 8 | 3.3 | 1102 | 2 | JH0717 | guanylate cyclase |
| 39 | 8 | 3.3 | 1108 | 2 | A55915 | guanylate cyclase |
| 40 | 8 | 3.3 | 1120 | 2 | H88449 | protein F54D8.1 (I) |
| 41 | 8 | 3.3 | 1265 | 1 | A37967 | neural cell adhesi |
| 42 | 8 | 3.3 | 1278 | 2 | T30188 | Niemann-Pick C dis |
| 43 | 8 | 3.3 | 1388 | 2 | A53317 | collagen alpha 1(X) |
| 44 | 8 | 3.3 | 1414 | 1 | S23809 | collagen alpha 2(I) |
| 45 | 8 | 3.3 | 1433 | 2 | A46053 | bullous pemphigoid |

ALIGNMENTS

RESULT 1
S57038
probable membrane protein YJR023c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 03-Jul-2004
C/Accession: S57038; S57041; S55212
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57038
A:Molecule type: DNA
A:Residues: 1-133 <ZAG>
A:Cross-references: UNIPROT:P47094; EMBL:249522; NID:g1015659; PID:g1015661
R:Zagulski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herber
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57040
A:Accession: S57041
A:Molecule type: DNA
A:Residues: 1-93 <HDA>
A:Cross-references: EMBL:249522; MIPS:YJR023C
R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A:Reference number: S55183
A:Accession: S55212
A:Molecule type: DNA
A:Residues: 1-133 <DEH>
A:Cross-references: EMBL:X87611
C:Genetics:
A:Cross-references: SGD:S0003784
A:Map position: 10R
C:Superfamily: Saccharomyces probable membrane protein YJR023c
C:Keywords: transmembrane protein

Query Match 3.7%; Score 9; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 22 LLLLLLQL 30

RESULT 2
T18867
hypothetical protein CO2F4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18867
R:Cummings, P.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19034

A>Title: Structural characterization of N-terminal antigenic determinants in calf and hu
A|Reference number: A91193; MUID:72255334; PMID:4115172
A|Accession: A91193
A|Molecule type: protein
A|Residues: 1-19 RABD
A|Cross-references: UNIPROT:P02453
A|Experimental source: Ekin
A|Note: the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is conve
R|Fietzek, P.P.; Kuehn, K.
E|Eur. J. Biochem. 52, 77-82, 1975
A|Title: The covalent structure of collagen amino-acid sequence of the quacore hant

A:Reference number: A91229; MUID:7602320; PMID:1164916
 A:Accession: A91229
 A:Molecule type: Protein
 A:Residues: 20-145 <FE>
 A:Experimental source: Skin
 A:Note: Lys-103 is hydroxylated and binds glucosylgalactose
 R,Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
 EBS Lett. 26, 74-76, 1972

A:Reference number: A91387; NCBI accession number: A91387
A:Accession: A91387
Molecule type: protein
Residues: 146-294 <P>
Experimental source: skin
R:Pietrek, P.P.; Rexford, F.W.; Hopper, K.E.; Kuehn, K.
J. Biochem. 38:106-110, 1973

A:Title: The covalent structure of collagen. 2. The amino-acid sequence of alpha1-CB7 fr
A:Reference number: A91211, NUID:74086118, PMID:4359390
A:Accession: A91211
A:Molecule type: protein
A:Residues: 295-562 <FT3>
A:Experimental source: skin
R:Reidt, B.; Marx, K.V.D.; Rexrodt, F.; Kuehn, K.

A:Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues
 A:Reference number: A91201; PMID:73042276; PMID:4343808
 A:Accession: A91201
 A:Molecule type: protein
 A:Residues: 563-675 <MEN>
 A:Experimental source: skin
 A:Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuhn, K.

Eur. J. Biochem. 30, 163-168, 1972
 A:Title: The covalent structure of collagen. Amino acid sequence of peptide alpha1-CB6-C7
 A:Reference number: A1200; MUID:75042275; PMID:4343807
 A:Accession: A91200
 A:Molecule type: protein
 A:Residues: 676-758 <PI4>
 A:Experimental source: skin
 A>Note: Pro-726 index: skin

A: Amino acid sequence of the carboxyterminal nonhelical cross link region of tRNA^{Phe}.
R: Rautenberg, J., Levine, S., Hargrave, P., Fletterick, J., Drenth, J., and O'Leary,
 J. L. (1987) Proc. Natl. Acad. Sci. USA 84, 600-604.
F: Fletterick, J., Drenth, J., and O'Leary, J. L. (1987) Biochemistry 26, 159-162.
K: Kuhn, M., and Becke, U. J. (1987) FEBS Lett. 21, 75-79.
T: Title, The amino acid sequence of the carboxyterminal nonhelical cross link region of tRNA^{Phe}.
Accession: A33048
Molecular type: protein
Residues: 759-779 <RA2>

A:Experimental source: skin
 Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydroxy
 Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are h
 Comment: The order of the eight CNR peptides in the alpha 1(I) chain of bovine skin c
 149, 266, and 217 residues.
 Comment: The complete chain contains 1052 residues.
 Keywords: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 Repeats: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 3.7%; Score 9; DB 1; Length 779;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 63 PGRDSEPGA 71
 |||||||||

DB 586 FGRDGPSCA 594

RESULT 5

JB0237

Apolipoprotein E receptor 2 precursor - mouse

N:Alternate names: apoER2

C:Species: Mus musculus (house mouse)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 03-Jul-2004

C:Accession: JB0237

R:Kim, H.J.; Kim, D.H.; Magoori, K.; Saeki, S.; Yamamoto, T.T.

J. Biochem. 124, 451-456, 1998

A:Title: Evolution of the apolipoprotein E receptor 2 gene by exon loss.

A:Reference number: JB0237; MUID:98352008; PMID:9685741

A:Accession: JB0237

A:Molecule type: mRNA

A:Residues: 1-996 <KIM>

A:Cross-references: UNIPROT:Q924X6; DDBJ:D85463

C:Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;

C:Keywords: glycoprotein

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-996/Product: apolipoprotein E receptor 2 #status predicted <MAT>

F:41-75/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:80-116/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:121-157/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:161-195/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:200-237/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F:251-286/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F:291-325/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F:331-368/Domain: LDL receptor ligand-binding repeat homology <LDL>

F:373-407/Domain: EGF homology <EGF>

F:585-628/Domain: LDL receptor WVTD-containing repeat homology <WVT>

F:723-767/Domain: EGF homology <EGF>

F:805-881/Domain: transmembrane #status predicted <TM>

F:805,840/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 3.7% Score 9; DB 2; Length 996;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 9; Mismatch 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24

DB 14 LLLLLLQL 22

RESULT 6

CGHUIS

collagen alpha 1(I) chain precursor - human

N:Alternate names: procollagen alpha 1(I) chain

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C:Accession: I60114; S01143; A93335; I55254; A39943; I55237; A55233; S09400; B90567; S115269; A29439; I53466; A02852; I37247

R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.

Gene 67, 105-115, 1988

A:Title: Complete nucleotide sequence of the region encompassing the first twenty-five

A:Reference number: I60114; MUID:88329734; PMID:284332

A:Accession: I60114

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 'U', 371-589 <DAL>

A:Cross-references: UNIPROT:PO2452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q1896; UNIF

R:Tromp, G.; Kuitavani, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock

Biochem. J. 253, 919-922, 1988

A:Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human

A:Reference number: S01143; MUID:89025644; PMID:3178743

A:Accession: S01143

A:Molecule type: mRNA

A:Residues: 1-472 <TRO>

A:Cross-references: EMBL:X07864; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID

A:Note: Submitted to the EMBL/GenBank/DBJ databases by Prockop, D.J., 13-JUN-1988

R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;

Nature 310, 337-340, 1984

A:Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of

A:Reference number: A93335; MUID:84270697; PMID:6462220

A:Accession: A93335

A:Molecule type: DNA

A:Residues: 1-58, 'O', 60-181 <CHU>

A:Cross-references: EMBL:X08820; NID:g35657; PIDN:CAA25394.1; PID:g35658

R:Rosouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.

J. Biol. Chem. 262, 15151-15157, 1987

A:Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh

A:Reference number: I55254; MUID:88033098; PMID:2822714

A:Accession: I55254

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-45 <ROS>

A:Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388

R:Bornstein, P.; McKay, J.; Morishima, J.K.; Devareyalu, S.; Gellinas, R.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987

A:Title: Regulatory elements in the first intron contribute to transcriptional control of

A:Reference number: A39943; MUID:88097389; PMID:3480516

A:Accession: A39943

A:Molecule type: DNA

A:Residues: 1-34 <BOR>

A:Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238

R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

J. Biol. Chem. 260, 2315-2320, 1985

A:Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter st

A:Reference number: I55237; MUID:85130970; PMID:2857713

A:Accession: I55237

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-34 <CH2>

A:Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226

R:Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holliste

J. Biol. Chem. 265, 6312-6317, 1990

A:Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-terminal

A:Reference number: A35233; MUID:90202908; PMID:2318855

A:Accession: A35233

A:Molecule type: protein

A:Residues: 33-52 <WIR>

A:Note: This propeptide fragment remained non-covalently bound to a defective, uncleaved

R:Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.

EMBO J. 8, 1705-1710, 1989

A:Title: A base substitution in the exon of a collagen gene causes alternative splicing

A:Reference number: S09400; MUID:89356643; PMID:2767050

A:Accession: S09400

A:Molecule type: mRNA

A:Residues: 156-183 <WEI>

R:Click, E.M.; Bornstein, P.

Biochemistry 9, 4639-4706, 1970

A:Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1

A:Reference number: A90567; MUID:71038625; PMID:5529814

A:Contents: CNBR0-1, CNBR2, CNBR4, CNBR5

A:Accession: B90567

A:Molecule type: protein

A:Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z',

A:Experimental source: skin

R:Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P.

Eur. J. Biochem. 192, 153-159, 1990

A:Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle

A:Reference number: S11372; MUID:90382436; PMID:2169412

A:Accession: S11372

A:Molecule type: protein

A:Residues: 175-187, 274-287, 'P', 289 <BAE>

A:Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion

R:Beak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzli, S.A.; Gonzalez

J. Biol. Chem. 266, 21827-21832, 1991

A:Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain

A:Reference number: I55342; MUID:92042092; PMID:1718984

A:Accession: I55342

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 258-268/1347-1357 <DBA>
 A:Cross-references: GB:S67495; NID:9239007; PIDN:AA20350.1; PID:9239008
 A>Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
 R:Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
 J. Biol. Chem. 245, 5042-5048, 1970
 A>Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
 A:Reference number: A92069; MUID:71001508; PMID:4319110
 A:Accession: A92069
 A:Molecule type: protein
 A:Residues: 263-268 <MOR>
 A:Experimental source: skin
 A>Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
 R:Labhard, M.E.; Hollister, D.W.
 Matrix 10, 124-130, 1990
 A>Title: Segmental amplification of the entire helical and telopeptide regions of the CT
 A:Reference number: S15989; MUID:90326017; PMID:2374517
 A:Accession: S15989
 A:Molecule type: mRNA
 A:Residues: 281-302/402-420/823-843/925-944/1026-1045/1143-1162 <LAB>
 R:Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.
 Connect. Tissue Res. 29, 1-11, 1993
 A>Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
 A:Reference number: 152905; MUID:9339042; PMID:8339541
 A:Accession: 152905
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 342-352, 'C', 354-359 <W12>
 A:Cross-references: GB:S64117; NID:9408195; PIDN:AA27677.1; PID:9408196
 A>Note: mutant sequence from patient with osteogenesis imperfecta
 R:Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Ellemerry, E.F.; Prockop, D.J.
 Biochemistry 22, 5213-5223, 1983
 A>Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1
 A:Reference number: A90476; MUID:84080385; PMID:6689127
 A:Accession: A90476
 A:Molecule type: mRNA
 A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1397-1464 <BER>
 A:Cross-references: GB:K01228; NID:9180391; PIDN:AA51995.1; PID:9180392
 A>Note: sequence partially completed for missing nucleotides by A93439
 R:Chu, M.L.; Gargiulo, V.; Williams, C.O.; Ramirez, F.
 J. Biol. Chem. 260, 691-694, 1985
 A>Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type II
 A:Reference number: A22161; MUID:85104934; PMID:2981843
 A:Accession: A22161
 A:Molecule type: DNA
 A:Residues: 472-594, 'R', 596-607 <CH3>
 A:Cross-references: GB:K03178; GB:K03179; NID:9179612; NID:9179613; PIDN:AA51847.1; PID
 R:Wallis, G.A.; Starman, B.J.; Zimm, A.B.; Byers, P.H.
 Am. J. Hum. Genet. 46, 1034-1040, 1990
 A>Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
 A:Reference number: A35336; MUID:90252792; PMID:2339700
 A:Accession: A35336
 A:Molecule type: mRNA
 A:Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
 A>Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
 R:Forlino, A.; Zollezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
 Hum. Mol. Genet. 3, 2201-2206, 1994
 A>Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the C
 A:Reference number: 154365; MUID:95187161; PMID:7881420
 A:Accession: 154365
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 746-766, 'S', 768-781 <FOR>
 A:Cross-references: GB:L47667; NID:91009093; PIDN:AA59576.1; PID:91009094
 R:Chesler, S.D.; Wallis, G.A.; Byers, P.H.
 J. Biol. Chem. 268, 18218-18225, 1993
 A>Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
 A:Reference number: A47426; MUID:93352646; PMID:8349697
 A:Accession: A47426
 A:Molecule type: mRNA
 A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>

A:Cross-references: GB:S64596; NID:9407589; PIDN:AA27856.1; PID:9407590
 A>Note: sequence extracted from NCBI backbone (NCBI:136444, NCBI:P:136445)
 A>Note: does not represent an experimentally determined sequence but three different mult
 A:Accession: B47426
 A:Molecule type: mRNA
 A:Residues: 1179-1464 <CH4>
 A:Experimental source: normal dermal fibroblast culture
 A:Accession: C47426
 A:Molecule type: mRNA
 A:Residues: 1179-1276, 'H', 1278-1464 <CH5>
 A:Experimental source: fetal cell 86-237
 A:Accession: D47426
 A:Molecule type: mRNA
 A:Residues: 1179-1336, 1339-1464 <CH6>
 A:Experimental source: fetal cell 86-146
 A:Accession: E47426
 A:Molecule type: mRNA
 A:Residues: 1179-1387, 'R', 1389-1464 <CH7>
 A:Experimental source: fetal cell 88-251
 R:Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nicl
 J. Biol. Chem. 263, 14605-14607, 1988
 A>Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of
 A:Reference number: 155269; MUID:89008319; PMID:3170557
 A:Accession: 155269
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1187-1194, 'C', 1196-1220 <COH>
 A:Cross-references: GB:M23213; NID:9340842; PIDN:AA59363.1; PID:9499622
 A>Note: mutant sequence from a patient with mild osteogenesis imperfecta
 R:Maehle, J.K.; Raasina, M.; Virta, A.; Vuorio, E.
 Nucleic Acids Res. 16, 349, 1988
 A>Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 PGRDGPQA 71
 DB 1024 PGRDGPQA 1032
 RESULT 7
 A60111
 sporozite antigen - Elmeria tenella (fragment)
 C:Species: Elmeria tenella
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 17-Jul-1994
 C:Accession: A60111
 R:Miller, G.A.; Bhogal, B.S.; McCandless, R.; Strauberg, R.L.; Jessee, E.J.; Anderson, J
 Infect. Immun. 57, 2014-2020, 1989
 A>Title: Characterization and vaccine potential of a novel recombinant coccidial antigen.
 A:Reference number: A60111; MUID:89277516; PMID:2659532
 A:Accession: A60111
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <ML>
 Query Match
 3.3%; Score 8; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 LLLLLLQ 23
 DB 3 LLLLLLQ 10
 RESULT 8
 LUTRUB
 lutropin beta chain precursor [validated] - human
 N:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing h
 C:Species: Homo sapiens (man)
 C:Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
 C:Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552

R:Palma, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin and
 A:Reference number: I37231; PMID:84093590; PMID:6690982
 A:Accession: I37994
 A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual transla
 A:Molecule type: DNA
 A:Residues: 1-141 <PAL>
 A:Cross-references: UNIPROT:P01229; GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
 R:Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jamieson, J.L.
 N. Engl. J. Med. 326, 179-183, 1992
 A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
 A:Reference number: I58013; PMID:92085985; PMID:127547
 A:Accession: I58013
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 72-73, 'R', 75-76 <WEI>
 A:Cross-references: GB:S71273; NID:g240572; PIDN:AAD14960.1; PID:g4262812
 A:Note: mutant sequence from patient with hypogonadism
 R:Saitam, M.R.; Li, C.H.
 Biochim. Biophys. Acta 412, 70-81, 1975
 A:Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
 A:Reference number: A90604; PMID:76062547; PMID:1191677
 A:Accession: A90604
 A:Molecule type: protein
 A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SAI>
 R:Shome, B.; Parlow, A.F.
 J. Clin. Endocrinol. Metab. 36, 618-621, 1973
 A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary
 A:Reference number: A92759; PMID:73090987; PMID:4685398
 A:Accession: A92759
 A:Molecule type: protein
 A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>
 R:Cloisset, J.; Hennen, G.; Leguin, R.M.
 FEBS Lett. 29, 97-100, 1973
 A:Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
 A:Reference number: A91389; PMID:73221227; PMID:4719207
 A:Contents: annotation; partial sequence
 R:Ward, D.N.
 unpublished results, cited by Cloisset, J., Hennen, G., and Leguin, R.M., FEBS Lett. 29,
 A:Reference number: A94466
 A:Accession: A94466
 A:Molecule type: protein
 A:Residues: 21-38, 'Q', 40-46 <WAR>
 A:Note: 28-Val, 33-Arg, and 35-Thr were also found
 R:Shome, B.; Parlow, A.F.
 submitted to the Atlas, April 1975
 A:Reference number: A94552
 A:Contents: annotation; binding site
 C:Genetics:
 A:Gene: GDB:LHB
 A:Cross-references: GDB:119364; OMIM:152780
 A:Map position: 19q13.3-19q13.3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: blocked amino end; status: protein; hormone: pituitary
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-141/Product: lutropin beta #status predicted <LUT>
 F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
 F:29-54, 42-77, 46-108, 58-130, 92-110, 110-113/Disulfide bonds: #status predicted
 F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GULLLLLLL 22
 |||||
 Db 6 GULLLLLLL 13

RESULT 9
 KTRUB
 choriongonadotropin beta chain precursor [validated] - human

N:Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
 C:Species: Homo sapiens (man)
 C:Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004
 C:Accession: A92230; 169972; I55224; I55250; I70007; I70008; A92303; A92181; A92142; PC1
 R:Fiddes, J.C.; Goodman, H.M.
 Nature 286, 684-687, 1980
 A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution
 A:Reference number: A92230; PMID:81012134; PMID:6774259
 A:Accession: A92230
 A:Molecule type: mRNA
 A:Residues: 1-165 <FID>
 A:Cross-references: UNIPROT:P01233; GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:A
 R:Pollicastro, P.; Ovit, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
 J. Biol. Chem. 258, 11492-11499, 1983
 A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple genes.
 A:Reference number: I55224; PMID:84008141; PMID:6194155
 A:Accession: I69972
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-165 <POL>
 A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
 A:Note: clone CG-beta-e
 A:Accession: I55224
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23, 'M', 25-136, 'A', 138-165 <PO2>
 A:Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
 A:Note: clone CG-beta-a
 R:Pollicastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
 J. Biol. Chem. 261, 5907-5916, 1986
 A:Title: A map of the hCG beta-LH beta gene cluster.
 A:Reference number: I55250; PMID:86195987; PMID:2422163
 A:Accession: I55250
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO3>
 A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
 A:Note: CG-beta-3 gene
 A:Accession: I70007
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO4>
 A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
 A:Note: CG-beta-6 gene
 A:Accession: I70008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <RES>
 A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090
 A:Note: CG-beta-7 gene
 R:Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
 J. Biol. Chem. 256, 1816-1823, 1981
 A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
 A:Reference number: A92303; PMID:8117268; PMID:7462224
 A:Accession: A92303
 A:Molecule type: protein
 A:Residues: 1-20 <BIR>
 A:Note: the identity of the residue at position 19 could not be determined
 R:Morgan, P.J.; Birken, S.; Canfield, R.E.
 J. Biol. Chem. 250, 5247-5258, 1975
 A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and t
 A:Reference number: A92181; PMID:75211304; PMID:1150658
 A:Accession: A92181
 A:Molecule type: protein
 A:Residues: 21-165 <MOR>
 R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
 J. Biol. Chem. 248, 6810-6827, 1973
 A:Reference number: A92142; PMID:74011267; PMID:4795659
 A:Accession: A92142
 A:Molecule type: protein
 A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP', <CAR>
 R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
 Chinese Biochem. J. 6, 558-562, 1990

A>Title: The immunological characteristics of the enzymatic fragments of human chorionic
 A/Reference number: PCI016
 A/Accession: PCI016
 A/Molecule type: protein
 A/Residues: 21-165 <SHT>
 A/Note: article in Chinese with English abstract
 R/Birken, S.; Armstrong, B.G.; Kolke, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
 Endocrinology 123, 572-583, 1988
 A/Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
 A/Reference number: A61097; MUID:88254680; PMID:2454811
 A/Accession: A61097
 A/Molecule type: protein
 A/Residues: 26-32,'X',34-49,'X',51-60,'75-112 <B12>
 A/Note: this material from pregnancy urine lacks static acid in its carbohydrate and has
 R/Kardana, A.; Bagshaw, K.D.; Cole, B.; Read, D.; Taylor, M.
 Br. J. Cancer 67, 686-692, 1993
 A/Title: Characterisation of UGP and its relationship with beta-core fragment.
 A/Reference number: A56873; MUID:93229246; PMID:8471426
 A/Accession: B56873
 A/Molecule type: protein
 A/Residues: 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48,'75-76,'X',78-91,'G',93-102 <KD
 A/Experimental source: urine
 A/Note: sequence modified after extraction from NCBI backbone
 A/Note: this material was designated urinary gonadotropin peptide (peak 2)
 R/Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Luebber, J.W.; Canfield, R.E.; Machin,
 Nature 369, 455-461, 1994
 A/Title: Crystal structure of human chorionic gonadotropin.
 A/Reference number: A44674; MUID:94261179; PMID:8202136
 R/Tilmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A/Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
 A/Reference number: I37231; MUID:84093590; PMID:6630962
 A/Accession: I37412
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: DNA
 A/Residues: 21-165 <RES>
 A/Cross-references: EMBL:X00265; NID:G31719; PIDN:CAA25068.1; PID:G1335075
 C/Genetics:
 A/Gene: GDB:CGB
 A/Cross-references: GDB:119055; OMIM:118860
 A/Map position: 19q13.3-19q13.3
 A/Introns: 5/3; 61/3
 A/Note: the choriongonadotropin beta chain locus contains six genes (or pseudogenes)
 C/Superfamily: pituitary glycoprotein hormone beta chain
 C/Keywords: glycoprotein; hormone; pituitary
 F.1-20/Domain: signal sequence #status experimental <SIG>
 F.21-165/Product: choriongonadotropin beta chain #status experimental <MAT>
 F.29-77/43-92,46-110,54-108,58-110,113-120/Disulfide bonds: #status experimental
 F.33.50/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.138.150/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F.141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GILLALL 22
 |||||
 |||||
 |||||
 |||||
 Db 6 GILLALL 13

RESULT 10
 T18321
 hypothetical protein L7610.12 - Leishmania major
 C/Species: Leishmania major
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
 C/Accession: T18321
 R/Oliver, K.; Murphy, L.; O'Neill, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
 submitted to the EMBL Data Library, May 1999
 A/Reference number: Z18876
 A/Accession: T18321
 A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA
 A/Residues: 1-169 <OLI>
 A/Cross-references: EMBL:AL034356; NID:el371878; PIDN:CAA2247.1
 C/Genetics:
 A/Note: L7610.12

Query Match 3.3%; Score 8; DB 2; Length 169;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PASPQRL 13
 |||||
 |||||
 |||||
 |||||
 Db 18 PASPQRL 25

RESULT 11
 S37749
 collagen alpha 2(XIV) chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: S37749
 R/Brown, J.C.; Goldik, R.; Mann, K.; Timpl, R.
 submitted to the EMBL Data Library, October 1993
 A/Description: Structure and stability of the triple helical domains of human collagen XI
 A/Reference number: S37749
 A/Accession: S37749
 A/Molecule type: protein
 A/Residues: 1-177 <BRO>
 A/Cross-references: UNIPROT:Q9UNP6
 C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
 ed and subsequently O-glycosylated.
 C/Genetics:
 A/Gene: COL14A2
 C/Complex: type XIV collagen may be a heterotrimer of alpha 1(XIV) chains and one alpha 2

A/Function:
 A/Description: structural component of extracellular fibrous polymer associated with coll
 C/Keywords: coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
 F.9,24,39,45,59,62,74,80,86,92,98,106,109,116,119,122,137,140/Modified site: 4-hydroxypr
 F.12/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F.18,143/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
 F.18,27,143/Binding site: carbohydrate (Lys) (covalent) #status experimental
 F.27/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 3.3%; Score 8; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 PGRDSPG 70
 |||||
 |||||
 |||||
 |||||
 Db 86 PGRDSPG 93

RESULT 12
 T35724
 cobalt transport integral membrane protein - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C/Accession: T35724
 R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: Z21548
 A/Accession: T35724
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: DNA
 A/Residues: 1-249 <MUR>
 A/Cross-references: UNIPROT:O54188; EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCODE
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: cbjQ, SCODEB:SC7H1.29C
 C/Superfamily: cobalt transport protein Q homolog

Query Match 3.3%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 GPAGVPR 65
 |||||
 Db 54 GPAGVPR 61

RESULT 13

138427
 4-1BB ligand - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I38427
 R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R
 Bur, J. Immunol. 24, 2219-2227, 1994
 A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
 A:Reference number: I38426; PMID:94374434; PMID:8088337
 A:Accession: I38427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-254 <RES>
 A:Cross-references: UNIPROT:P41273; EMBL:U03398; NID:G571322; PIDN:AAA53134.1; PID:G5713

Query Match 3.3%; Score 8; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GLLLLLL 22
 |||||
 Db 34 GLLLLLL 41

RESULT 14

B60131
 homeotic protein Xhox-7.1' - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Aug-2004
 C:Accession: B60131; S14514
 R:Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
 Development 111, 1179-1187, 1991
 A:Title: Progressively restricted expression of a new homeobox-containing gene during Xe
 A:Reference number: A60131; PMID:91347929; PMID:1679007
 A:Accession: B60131
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-9, 'P', 11-291 <SUA>
 A:Cross-references: UNIPROT:P35993; EMBL:X58772
 R:Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F.
 submitted to the EMBL Data Library, December 1990
 A:Reference number: S14513
 A:Accession: S14514
 A:Molecule type: mRNA
 A:Residues: 1-291 <SUA2>
 A:Cross-references: EMBL:X58772; NID:G64784; PIDN:CAA41573.1; PID:G64785
 C:Superfamily: homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:161-217/Domain: homeobox homology <HOK>

Query Match 3.3%; Score 8; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLLQ 23
 |||||
 Db 6 LLLLLLLQ 13

RESULT 15

T24827
 hypothetical protein T11B7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24827

R:Gardner, A.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: Z19940
 A:Accession: T24827

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-296 <WIL>
 A:Cross-references: UNIPROT:Q22389; EMBL:Z54237; PIDN:CAA90989.1; GSPDB:GN00022; CESP:T11
 A:Experimental source: clone T11B7
 C:Genetics:
 A:Gene: CESP:T11B7.3
 A:Map position: 4
 A:introns: 45/3; 111/1; 270/1

Query Match 3.3%; Score 8; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 PGIPGRDG 85
 |||||
 Db 266 PGIPGRDG 273

Search completed: December 25, 2004, 05:33:23
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:26:21 ; Search time 95 Seconds
(without alignments)
1471.748 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 243

Sequence: 1 MRPGPASPQRRLGILL...GDASTGMSVSRRIIEELPK 243

Scoring table: ~~40EBCG~~
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size: 6

Total number of hits satisfying chosen parameters: 11652

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 243 | 100.0 | 243 | 2 | 06UW91 |
| 2 | 243 | 100.0 | 243 | 2 | AA089273 |
| 3 | 170 | 70.0 | 243 | 2 | 096CG8 |
| 4 | 169 | 69.5 | 232 | 2 | 081X63 |
| 5 | 111 | 45.7 | 245 | 2 | 08CG08 |
| 6 | 111 | 45.7 | 245 | 2 | 09DID6 |
| 7 | 9 | 3.7 | 53 | 2 | 06H8C6 |
| 8 | 9 | 3.7 | 86 | 2 | 06IH72 |
| 9 | 9 | 3.7 | 86 | 2 | 06IUS3 |
| 10 | 9 | 3.7 | 96 | 2 | 06IOT6 |
| 11 | 9 | 3.7 | 105 | 2 | 06IG45 |
| 12 | 9 | 3.7 | 120 | 1 | GON2_HUMAN |
| 13 | 9 | 3.7 | 120 | 2 | AAH65362 |
| 14 | 9 | 3.7 | 133 | 1 | YJ23_YEAST |
| 15 | 9 | 3.7 | 144 | 2 | P90741 |
| 16 | 9 | 3.7 | 163 | 2 | 06ILM0 |
| 17 | 9 | 3.7 | 191 | 2 | 06ILU4 |
| 18 | 9 | 3.7 | 205 | 1 | RNS9_CEBCA |
| 19 | 9 | 3.7 | 274 | 2 | 080YU5 |
| 20 | 9 | 3.7 | 299 | 2 | 06IIF0 |
| 21 | 9 | 3.7 | 324 | 2 | 07NFG2 |
| 22 | 9 | 3.7 | 384 | 2 | 07XEC4 |
| 23 | 9 | 3.7 | 472 | 2 | 06BOD7 |
| 24 | 9 | 3.7 | 501 | 2 | 09AVM0 |
| 25 | 9 | 3.7 | 558 | 2 | 09ASN8 |
| 26 | 9 | 3.7 | 779 | 1 | CA11_BOVIN |
| 27 | 9 | 3.7 | 813 | 1 | CADW_RAT |
| 28 | 9 | 3.7 | 896 | 1 | ATIS_MOUSE |
| 29 | 9 | 3.7 | 996 | 1 | LRP8_MOUSE |
| 30 | 9 | 3.7 | 1069 | 2 | 06LAN8 |
| 31 | 9 | 3.7 | 1069 | 2 | CAAG7261 |

| | | | | | | |
|----|---|-----|------|---|------------|--------------------|
| 32 | 9 | 3.7 | 1348 | 2 | 07PYX1 | Q7PYX1 anopheles g |
| 33 | 9 | 3.7 | 1461 | 2 | 076045 | O76045 homo sapien |
| 34 | 9 | 3.7 | 1464 | 1 | CA11_HUMAN | P02452 homo sapien |
| 35 | 9 | 3.7 | 1464 | 2 | 08N473 | O8N473 homo sapien |
| 36 | 9 | 3.7 | 1464 | 2 | 06P912 | Q6P912 xenopus lae |
| 37 | 9 | 3.7 | 1464 | 2 | AAH60753 | AAH60753 xenopus t |
| 38 | 9 | 3.7 | 1492 | 2 | 06P422 | Q6P422 xenopus t |
| 39 | 9 | 3.7 | 1492 | 2 | AAH63191 | AAH63191 xenopus t |
| 40 | 8 | 3.3 | 59 | 2 | 08K312 | O8K312 mus musculu |
| 41 | 8 | 3.3 | 65 | 2 | 08K312 | Q8K312 mus musculu |
| 42 | 8 | 3.3 | 79 | 2 | 06K251 | Q6K251 oryza sativ |
| 43 | 8 | 3.3 | 79 | 2 | BAD20061 | BAD20061 oryza sat |
| 44 | 8 | 3.3 | 79 | 2 | BAD20107 | BAD20107 oryza sat |
| 45 | 8 | 3.3 | 108 | 2 | Q9D9P8 | Q9D9P8 mus musculu |

ALIGNMENTS

| RESULT 1 | ID | 06UW91 | PRELIMINARY | PRT | 243 AA. |
|---------------------------|---|--|-------------|-----|---------|
| AC | 06UW91 | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Created) | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Last sequence update) | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Last annotation update) | | | | |
| DE | CTHRC1. | | | | |
| GN | ORFName=UNQ762; | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | | | |
| OX | NCBI_Taxid=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=22887296; PubMed=12975309; | | | | |
| RA | Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D., Brush J., | | | | |
| RA | Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., | | | | |
| RA | Raton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S., | | | | |
| RA | Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., | | | | |
| RA | Lewis L., Liao D., Mark W., Robble E., Sanchez C., Schoenfeld J., | | | | |
| RA | Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., | | | | |
| RA | Vandlen R., Watanabe C., Wiand D., Woode K., Xie M.H., Yansura D., | | | | |
| RA | Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., | | | | |
| RA | Godowski P.; | | | | |
| RT | "The secreted protein discovery initiative (SPDI), a large-scale | | | | |
| RT | effort to identify novel human secreted and transmembrane proteins: a | | | | |
| RT | bioinformatic assessment." | | | | |
| RL | Genome Res. 13:2265-2270(2003). | | | | |
| DR | EMBL; AY358914; AA089273.1; -. | | | | |
| DR | InterPro; IPR008161; Clg_helix. | | | | |
| DR | InterPro; IPR008160; Collagen. | | | | |
| DR | ProDom; PD000007; Clg_helix; 1. | | | | |
| KW | COLLAGEN. | | | | |
| SQ | SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC303BC CRC64; | | | | |
| Query Match | 100.0%; Score 243; DB 2; Length 243; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 1.6e-220; Mismatches 0; | | | | |
| Matches 243; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 1 | MRPGPASPQRRLGILLQLLPASASRIIPGKOKAOLRREVVLDLNGMCLOGPA | 60 | | |
| DB | 1 | MRPGPASPQRRLGILLQLLPASASRIIPGKOKAOLRREVVLDLNGMCLOGPA | 60 | | |
| QY | 61 | GVPRGDSFGANVIGTPTGIPGRDQKGEKGLRESEFSESTPYKQCSWSLNYGIDL | 120 | | |
| DB | 61 | GVPRGDSFGANVIGTPTGIPGRDQKGEKGLRESEFSESTPYKQCSWSLNYGIDL | 120 | | |
| QY | 121 | GKIAECTPTKMSNSALRLVFGSLRLKCRNACCGRWFTFGAGCSGFLPEATIIYLDQ | 180 | | |
| DB | 121 | GKIAECTPTKMSNSALRLVFGSLRLKCRNACCGRWFTFGAGCSGFLPEATIIYLDQ | 180 | | |
| QY | 181 | GSPENNSTIHRTSSVEGLCEGIGLVDAIWWGTCSDYPKGDASTGMSVSRRIIEE | 240 | | |
| DB | 181 | GSPENNSTIHRTSSVEGLCEGIGLVDAIWWGTCSDYPKGDASTGMSVSRRIIEE | 240 | | |

Db 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRILIEE 240
 Qy 241 LPK 243
 ||||
 Db 241 LPK 243

RESULT 2
 AAQ89273 PRELIMINARY; PRT; 243 AA.

AC AAQ89273; TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE CTRHCL.
 GN UNO762.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gurely A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang L., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simons L., Singh V., Stinson J., Vagstad A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yarusla A.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 DR EMBL: AY358914; AAQ89273.1; -;
 SQ SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC03BC CRC64;

Query Match 100.0%; Score 243; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.6e-220;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPQGPASFORLRLGLLILLLILQLPAPSSASELPKQKQXOLRORVNDLYNMCLOQPA 60
 Db 1 MRPQGPASFORLRLGLLILLLILQLPAPSSASELPKQKQXOLRORVNDLYNMCLOQPA 60
 Qy 61 GVPGRGSPGANVTPGTPIPGRDGFKGKGECLARESPESWTPNYKQCSMSLNYGIDL 120
 Db 61 GVPGRGSPGANVTPGTPIPGRDGFKGKGECLARESPESWTPNYKQCSMSLNYGIDL 120
 Qy 121 GIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYTFENGACSGPLPEAIIYIDQ 180
 Db 121 GIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYTFENGACSGPLPEAIIYIDQ 180
 Qy 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRILIEE 240
 Db 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRILIEE 240
 Qy 241 LPK 243
 ||||
 Db 241 LPK 243

RESULT 3
 Q96CG8 PRELIMINARY; PRT; 243 AA.
 AC Q96CG8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Collagen triple helix repeat containing 1 (Collagen triple helix repeat-containing protein 1).

GN Name=CTHRC1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg S.B., Buetow K.H., Scheet C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., Mesman P.J., McKernan K.J., Alek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Helton E., Kettelman M., Madan A., Rodriguez G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smaltis D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Wai M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta smooth muscle;
 RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014245; AAI14245.1; -;
 DR EMBL: AY136825; AANI5749.1; -;
 DR Genew; HGNC:18831; CTRHCL.
 DR GO: GO:0005737; C:cytoplasm; IEA.
 DR GO: GO:0006817; P:phosphate transport; IEA.
 DR InterPro: IPR008161; Clg_helix.
 DR InterPro: IPR008160; Collagen.
 DR Pfam: PF01391; Collagen; 1.
 DR ProDom: PD000007; Clg_helix; 1.
 DR K4
 SQ SEQUENCE 243 AA; 26224 MW; A1FFEB1C66867F9 CRC64;

Query Match 70.0%; Score 170; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.1e-151;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 IPGTPIPGRDGFKGKGECLARESPESWTPNYKQCSMSLNYGIDLGIAECTFTKMS 133
 Db 74 IPGTPIPGRDGFKGKGECLARESPESWTPNYKQCSMSLNYGIDLGIAECTFTKMS 133
 Qy 134 NSALRYLFGSGLRLKCRNACCORWYTFENGACSGPLPEAIIYIDQSGSPENNSTINIR 193
 Db 134 NSALRYLFGSGLRLKCRNACCORWYTFENGACSGPLPEAIIYIDQSGSPENNSTINIR 193
 Qy 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRILIEELK 243
 Db 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMSVSRILIEELK 243

RESULT 4
 Q81X63 PRELIMINARY; PRT; 232 AA.
 ID Q81X63;
 AC Q81X63;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE NTMCL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBD databases.
DR EMBL; AF395488; AA017919.1; -
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR ProDom; PD000007; Clg_helix; 1.
KW Collagen.
SQ SEQUENCE 232 AA; 25163 MW; E9D4BC30304837ED CRC64;

Query Match 69.5%; Score 169; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.4e-151;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IGTGPIGRDGFKEGKGLRESFESWTNNKQCSWSLNYGIDLGIAECTPTKMS 133
DB 60 IGTGPIGRDGFKEGKGLRESFESWTNNKQCSWSLNYGIDLGIAECTPTKMS 119
QY 134 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEALITYLDGSPENSTINHR 193
DB 120 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEALITYLDGSPENSTINHR 179
QY 194 TSSVGEGLCGIGAGLVDAVIAWGTGCDYRKGDASTGMSVSRITIELP 242
DB 180 TSSVGEGLCGIGAGLVDAVIAWGTGCDYRKGDASTGMSVSRITIELP 228

RESULT 5

Q8CG08 PRELIMINARY; PRT; 245 AA.
ID Q8CG08;
AC Q8CG08;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Collagen triple helix repeat-containing protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=8 day balloon-injured carotid artery;
RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBD databases.
DR EMBL; AY136824; AAM15748.1; -
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR ProDom; PD000007; Clg_helix; 1.
KW Collagen.
SQ SEQUENCE 245 AA; 26424 MW; 2296FD6DCDBA21F2 CRC64;

Query Match 45.7%; Score 111; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-96;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IGTGPIGRDGFKEGKGLRESFESWTNNKQCSWSLNYGIDLGIAECTPTKMS 133
DB 76 IGTGPIGRDGFKEGKGLRESFESWTNNKQCSWSLNYGIDLGIAECTPTKMS 135

QY 134 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEALITYLDGSP 184
DB 136 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEALITYLDGSP 186

RESULT 6

Q9D1D6 PRELIMINARY; PRT; 245 AA.
ID Q9D1D6;
AC Q9D1D6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014807 product:hypothetical Collagen triple helix repeat containing protein, full insert sequence.
DE repeat containing protein, full insert sequence.
GN Name=Ctrcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RA The FANTOM Consortium;
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RL "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RL "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arahawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK003674; BAB22930.1; -
 DR MGD; MGI:1915838; Cbrc1.
 DR GO; GO:0005737; C-tyclopasm. IEA.
 DR GO; GO:0006817; P-phosphatase transport; IEA.
 DR InterPro; IPR008161; C1g_helix.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen.1.
 DR ProDom; PD000007; C1g_helix.1.
 DR Collagen; Hypothetical protein.
 SQ SEQUENCE 245 AA; 26460 MW; 14951B87D8181A0E CRC64;

Query Match
 Best Local Similarity 45.7%; Score 111; DB 2; Length 245;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFGEKGEKLESEFEEWTPNYQCSSINYGIDIGKIAECTFTMRS 133
 |||||
 DB 76 IPGTGPIGRDGFGEKGEKLESEFEEWTPNYQCSSINYGIDIGKIAECTFTMRS 135
 |||||
 QY 134 NSALRVLPSSGLRLKRCNACCORWYFTFNGAECGSPLEPIEATILYLDGSPSE 184
 |||||
 DB 136 NSALRVLPSSGLRLKRCNACCORWYFTFNGAECGSPLEPIEATILYLDGSPSE 186
 |||||

RESULT 7
 O6H8C6 PRELIMINARY; PRT; 53 AA.
 AC O6H8C6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein OJ1006_A02.39.
 GN Name-OJ1006_A02.39.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003977; BAD25023.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 53 AA; 5363 MW; 7A0775BFC5C7A683 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 9; DB 2; Length 53;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLOL 24
 |||||
 DB 22 LLLLLLLOL 30
 |||||

RESULT 8
 O6IH72 PRELIMINARY; PRT; 86 AA.
 AC O6IH72;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE HDC03105.
 GN OryNames=HDC03105;
 OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=14709175;
 RA Hild M., Beckmann B., Haas S., Koch B., Solovjev V., Buesold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohenberg J., Pato R.,
 RT "An integrated gene annotation and transcriptional profiling approach
 towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK003544; DAA03743.1; -
 SQ SEQUENCE 86 AA; 9918 MW; E7E62A6DFAD94D40 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 9; DB 2; Length 86;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLOL 24
 |||||
 DB 39 LLLLLLLOL 47
 |||||

RESULT 9
 O6ILS3 PRELIMINARY; PRT; 86 AA.
 AC O6ILS3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE HDC08497.
 GN OryNames=HDC08497;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=14709175;
 RA Hild M., Beckmann B., Haas S., Koch B., Solovjev V., Buesold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohenberg J., Pato R.,
 RT "An integrated gene annotation and transcriptional profiling approach
 towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK001943; DAA02788.1; -
 SQ SEQUENCE 86 AA; 9651 MW; DBE5E1028C6A12B3 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 9; DB 2; Length 86;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLOL 24
 |||||
 DB 45 LLLLLLLOL 53
 |||||

RESULT 10
 O6IUT6 PRELIMINARY; PRT; 96 AA.
 AC O6IUT6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE HDC14245.
 GN OryNames=HDC14245;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Hild M., Beckmann B., Haas S., Koch B., Solov'ev V., Busold C.,
RX PubMed=14709175;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:R3-R3(2003).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK002630; DAA04136.1; -.
SQ SEQUENCE 96 AA; 11039 MW; BFCBICDCC3F1BEDD CRC64;

Query Match 3.7%; Score 9; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
| | | | | | |
Db 7 LLLLLLQL 15

RESULT 11
Q6IG45 PRELIMINARY; PRT; 105 AA.
AC Q6IG45;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HDC07244.
GN ORFNames=HDC07244;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha.
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Hild M., Beckmann B., Haas S., Koch B., Solov'ev V., Busold C.,
RX PubMed=14709175;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:R3-R3(2003).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK003921; DAA02619.1; -.
SQ SEQUENCE 105 AA; 11424 MW; F655A4D40747519D CRC64;

Query Match 3.7%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
| | | | | | |
Db 14 LLLLLLQL 22

RESULT 12
CON2_HUMAN STANDARD; PRT; 120 AA.
AC Q4355; Q9BYN9; Q9BYR0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gonadoliberin II precursor [Contains: Gonadoliberin II (LH-RH II)
DE (Luteinizing hormone-releasing hormone II) (Gonadorelin-releasing
DE hormone II) (GHRH II) (Luliberin II); GnRH-associated peptide II].
GN Name=GNRH2.
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98081869; PubMed=9419371;
RA White R.B., Eisen J.A., Kastan T.L., Fernald R.D.;
RT "Second gene for gonadotropin-releasing hormone in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:305-309(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/444865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Pavlidis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffith D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Humble E., Hunt A.R., Hunt S.E., Jekoson K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharvaslho M.H., Levarina M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.B.,
RA Swann R.M., Symons A.C., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Trecey A.R., Tyromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmink L., Wray P.M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RL "The DNA sequence and comparative analysis of human chromosome 20.";
RT Nature 414:865-871(2001).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=O43555-1; Sequence=displayed;
CC Name=2;
CC IsoId=O43555-2; Sequence=VSP_001825;
CC Name=3;
CC IsoId=O43555-3; Sequence=VSP_001826;
CC -1- TISSUE SPECIFICITY: Midbrain; expressed at significantly higher
CC levels outside the brain (up to 30-fold), particularly in the
CC kidney, bone marrow and prostate.
CC -1- SIMILARITY: Belongs to the GnRH family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF036329; AAC02980.1; -
CC EMBL; AF036330; AAC02981.1; -
CC EMBL; AL121905; CAC10338.1; -
CC EMBL; AL121905; CAC29100.1; -
CC EMBL; AL121905; CAC29101.1; -
CC Genew; HGNC:4420; GNHR2.
CC MIM; 602352; -

DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein C02F4.3.
GN Name=C02F4.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RL investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Cummings P.N.;
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81032; CAB02722.1; -.
DR PIR; T18867; T18867.
DR WormPep; C02F4.3; CE07854.
KW Hypothetical protein.
SQ SEQUENCE 144 AA; 16112 MW; 907F9DDB1ACC1762 CRC64;

Query Match 3.7%; Score 9; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLQL 24
 |||||
 |||||
Db 67 LLLLLLQL 75

Search completed: December 25, 2004, 05:32:53
Job time : 97 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 25, 2004, 05:31:17 ; Search time 497 Seconds
(without alignments)
2566.618 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MKPQPASPORTRLGILL.....GDASTGMSVSRITIEELPK 243

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:

-MODEL=frame+pn.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US10063734/runat_22122004.101733.8913/app_query.fasta_1.391
-DB=N Geneseq_23Sep04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
-NODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063734 @CGN_1_1470 @runat_22122004.101733.8913 -NCPu=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: N_Geneseq_23Sep04:*
2: geneseqn1908:*
3: geneseqn1908:*
4: geneseqn2000as:*
5: geneseqn2000as:*
6: geneseqn2002as:*
7: geneseqn2002as:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1301 | 100.0 | 729 | 6 | ABSG4029 Human bre |
| 2 | 1301 | 100.0 | 729 | 10 | ABT33241 Human tum |
| 3 | 1301 | 100.0 | 729 | 11 | ADU93173 Human bre |
| 4 | 1301 | 100.0 | 732 | 6 | ABV99144 Human pan |
| 5 | 1301 | 100.0 | 732 | 6 | ABSG4028 Human bre |
| 6 | 1301 | 100.0 | 732 | 10 | ABT33240 Human tum |

| | | | | | | |
|----|------|-------|------|----|----------|--------------------|
| 7 | 1301 | 100.0 | 732 | 11 | ADL93172 | Adl93172 Human bre |
| 8 | 1301 | 100.0 | 837 | 6 | ABV99145 | Abv99145 Human pan |
| 9 | 1301 | 100.0 | 837 | 6 | ABSG4030 | Absg4030 Human bre |
| 10 | 1301 | 100.0 | 837 | 6 | ABSG4031 | Absg4031 Human bre |
| 11 | 1301 | 100.0 | 837 | 10 | ABT33242 | Abt33242 Human tum |
| 12 | 1301 | 100.0 | 837 | 10 | ABT33243 | Abt33243 Human tum |
| 13 | 1301 | 100.0 | 837 | 11 | ADL93174 | Adl93174 Human bre |
| 14 | 1301 | 100.0 | 837 | 11 | ADL93175 | Adl93175 Human bre |
| 15 | 1301 | 100.0 | 1256 | 10 | ADB90997 | Adb90997 Novel hum |
| 16 | 1301 | 100.0 | 1257 | 3 | MAA37144 | Ma37144 Human PRO |
| 17 | 1301 | 100.0 | 1257 | 4 | MAF54507 | Ma54507 Probe #60 |
| 18 | 1301 | 100.0 | 1257 | 4 | MAA6107 | Ma6107 Human DNA |
| 19 | 1301 | 100.0 | 1257 | 4 | MAF92118 | Ma92118 Human PRO |
| 20 | 1301 | 100.0 | 1257 | 6 | ABT74438 | Abt74438 Human PRO |
| 21 | 1301 | 100.0 | 1257 | 6 | ABT88194 | Abt88194 Human PRO |
| 22 | 1301 | 100.0 | 1257 | 6 | MAA32717 | Ma32717 Human tum |
| 23 | 1301 | 100.0 | 1257 | 6 | ABU95683 | Abu95683 Human ang |
| 24 | 1301 | 100.0 | 1257 | 6 | ACA89557 | Ac89557 CDNA enco |
| 25 | 1301 | 100.0 | 1257 | 8 | ACA73567 | Ac73567 Human sec |
| 26 | 1301 | 100.0 | 1257 | 8 | ACA05882 | Ac05882 Human sec |
| 27 | 1301 | 100.0 | 1257 | 8 | ACA66716 | Ac66716 CDNA enco |
| 28 | 1301 | 100.0 | 1257 | 8 | ACA91224 | Ac91224 Novel hum |
| 29 | 1301 | 100.0 | 1257 | 8 | ACD81601 | Ac81601 Human CDN |
| 30 | 1301 | 100.0 | 1257 | 8 | ACF20291 | Ac20291 Human sec |
| 31 | 1301 | 100.0 | 1257 | 8 | ACF19677 | Ac19677 Human sec |
| 32 | 1301 | 100.0 | 1257 | 8 | ACD21965 | Ac21965 Human sec |
| 33 | 1301 | 100.0 | 1257 | 8 | ACR13130 | Ac13130 Human sec |
| 34 | 1301 | 100.0 | 1257 | 8 | ACD25233 | Ac25233 Human sec |
| 35 | 1301 | 100.0 | 1257 | 8 | ACF00282 | Ac00282 Human sec |
| 36 | 1301 | 100.0 | 1257 | 8 | ACA60423 | Ac60423 Novel hum |
| 37 | 1301 | 100.0 | 1257 | 8 | ACA72339 | Ac72339 Novel hum |
| 38 | 1301 | 100.0 | 1257 | 8 | ACD04863 | Ac04863 Novel hum |
| 39 | 1301 | 100.0 | 1257 | 8 | ACD18324 | Ac18324 Human sec |
| 40 | 1301 | 100.0 | 1257 | 8 | ACD08331 | Ac08331 Human sec |
| 41 | 1301 | 100.0 | 1257 | 8 | ACA88765 | Ac88765 Novel hum |
| 42 | 1301 | 100.0 | 1257 | 8 | ACA70207 | Ac70207 Human sec |
| 43 | 1301 | 100.0 | 1257 | 8 | ACD12429 | Ac12429 Novel hum |
| 44 | 1301 | 100.0 | 1257 | 8 | ACG74344 | Ac74344 Human sec |
| 45 | 1301 | 100.0 | 1257 | 8 | ACD15972 | Ac15972 Human sec |
| 46 | 1301 | 100.0 | 1257 | 8 | ACD25540 | Ac25540 Novel hum |
| 47 | 1301 | 100.0 | 1257 | 8 | ACD18017 | Ac18017 Human sec |
| 48 | 1301 | 100.0 | 1257 | 8 | ACD88304 | Ac88304 Human sec |
| 49 | 1301 | 100.0 | 1257 | 8 | ACD21658 | Ac21658 Human sec |
| 50 | 1301 | 100.0 | 1257 | 8 | ACD18725 | Ac18725 Human sec |
| 51 | 1301 | 100.0 | 1257 | 8 | ACA58870 | Ac58870 CDNA enco |
| 52 | 1301 | 100.0 | 1257 | 8 | ABX98335 | Abx98335 Human CDN |
| 53 | 1301 | 100.0 | 1257 | 8 | ACD14086 | Ac14086 Human PRO |
| 54 | 1301 | 100.0 | 1257 | 8 | ACD09866 | Ac09866 Human sec |
| 55 | 1301 | 100.0 | 1257 | 8 | ACC88611 | Ac88611 Human sec |
| 56 | 1301 | 100.0 | 1257 | 8 | ACD21351 | Ac21351 Human sec |
| 57 | 1301 | 100.0 | 1257 | 8 | ABX75723 | Abx75723 Human CDN |
| 58 | 1301 | 100.0 | 1257 | 8 | ACA64046 | Ac64046 CDNA enco |
| 59 | 1301 | 100.0 | 1257 | 8 | ABX97926 | Abx97926 Human PRO |
| 60 | 1301 | 100.0 | 1257 | 8 | ACA97402 | Ac97402 Novel hum |
| 61 | 1301 | 100.0 | 1257 | 8 | ACA57865 | Ac57865 Human PRO |
| 62 | 1301 | 100.0 | 1257 | 8 | ACD14393 | Ac14393 Human PRO |
| 63 | 1301 | 100.0 | 1257 | 8 | ACC91176 | Ac91176 Human sec |
| 64 | 1301 | 100.0 | 1257 | 8 | ACC88918 | Ac88918 Human sec |
| 65 | 1301 | 100.0 | 1257 | 8 | ACD07115 | Ac07115 Human PRO |
| 66 | 1301 | 100.0 | 1257 | 8 | ACA67566 | Ac67566 Human PRO |
| 67 | 1301 | 100.0 | 1257 | 8 | ACC81621 | Ac81621 Human sec |
| 68 | 1301 | 100.0 | 1257 | 8 | ACA91310 | Ac91310 CDNA enco |
| 69 | 1301 | 100.0 | 1257 | 8 | ACC89225 | Ac89225 Human sec |
| 70 | 1301 | 100.0 | 1257 | 8 | ACC86581 | Ac86581 Human sec |
| 71 | 1301 | 100.0 | 1257 | 8 | ACC89839 | Ac89839 Human sec |
| 72 | 1301 | 100.0 | 1257 | 8 | ACC93018 | Ac93018 Human sec |
| 73 | 1301 | 100.0 | 1257 | 8 | ACA72646 | Ac72646 Human PRO |
| 74 | 1301 | 100.0 | 1257 | 8 | ACA89164 | Ac89164 Human sec |
| 75 | 1301 | 100.0 | 1257 | 8 | ACA69900 | Ac69900 Human sec |
| 76 | 1301 | 100.0 | 1257 | 8 | ACA97043 | Ac97043 Novel hum |
| 77 | 1301 | 100.0 | 1257 | 8 | ACA91039 | Ac91039 Novel hum |
| 78 | 1301 | 100.0 | 1257 | 8 | ACA70821 | Ac70821 Human sec |
| 79 | 1301 | 100.0 | 1257 | 8 | ACA95331 | Ac95331 Novel hum |

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80 1301 100.0 1257 8 ACC86274 Acc86274 Human sec
81 1301 100.0 1257 8 ACC45209 Acc45209 Human sec
82 1301 100.0 1257 8 ACC90146 Acc90146 Human sec
83 1301 100.0 1257 8 ACC12754 Acc12754 Human sec
84 1301 100.0 1257 8 ACC19984 Acc19984 Human sec
85 1301 100.0 1257 8 ABX76928 ABX76928 Human sec
86 1301 100.0 1257 8 ACA73260 ACA73260 Human PRO
87 1301 100.0 1257 8 ACA68803 ACA68803 Novel hum
88 1301 100.0 1257 8 ACA74647 ACA74647 Novel hum
89 1301 100.0 1257 8 ACA70514 ACA70514 Human sec
90 1301 100.0 1257 8 ACC14700 Acc14700 Human PRO
91 1301 100.0 1257 8 ACA83757 ACA83757 Human CDN
92 1301 100.0 1257 8 ACA68372 ACA68372 Novel hum
93 1301 100.0 1257 8 ABX98837 ABX98837 Novel hum
94 1301 100.0 1257 8 ACA67331 ACA67331 CDNA enco
95 1301 100.0 1257 8 ACC81314 ACC81314 Human sec
96 1301 100.0 1257 8 ACA95638 ACA95638 Novel hum
97 1301 100.0 1257 8 ACCD04556 ACCD04556 Novel hum
98 1301 100.0 1257 8 ACC87997 ACC87997 Human sec
99 1301 100.0 1257 8 ACC12659 ACC12659 Human sec
100 1301 100.0 1257 8 ACH66304 ACH66304 Novel hum

```

ALIGNMENTS

```

RESULT 1
ABSE4029
ID ABSE4029 standard; cDNA; 729 BP.
XX
XX ABSE4029;
AC
XX 15-NOV-2002 (first entry)
XX
XX Human breast tumour polynucleotide #478.
DE
XX Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
KW vaccine.
XX
XX Homo sapiens.
XX
XX US2002085998-A1.
FN
XX
XX 04-JUL-2002.
PD
XX
XX 13-APR-2001; 2001US-00834759.
PE
XX
XX 28-DEC-1998; 98US-00222575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-0051621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX
XX (CORI-) CORIXA CORP.
PA
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI Henderson RA;
XX
XX WPI; 2002-635657/68.
DR P-PSDB; ABG78938.
XX
XX Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in a
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX
XX Claim 1; Page 234; 247pp; English.
XX
XX The invention relates to an isolated breast tumour polynucleotide and the
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC detecting the presence of breast cancer in a patient, and in

```

CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention

XX Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;

Alignment Scores:

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Pred. No.: 1,298-104 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

```

US-10-063-734-122 (1-243) x ABSE4029 (1-729)

```

QY 1 MetATGProGInGlyProAlaAlaSerProGInaArgLeuArgGlyLeuLeuLeu 20
DB 1 ATGCGACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGCCCTCGCTGCTCCTG 60
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla 40
DB 61 CTGCTGCGAGCTGCCCGCGCCCTCGAGCGCTCTGAGATCCCGAAGGGAAGCAAGGGCG 120
QY 41 GInLeuArgGInaArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGInGlyProAla 60
DB 121 CAGCTCCGCGCAGAGGAGGTGTGCACTGTATATATAGATGTGCTTACAGGGCCACGA 180
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 181 GGAGTGCTGTGTCAAGACGGAGGCTCGGGCCAAATGTTATTCGGGTACCTGGGATC 240
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 241 CCAGGTGGGATGATGATTCAAAGAGAAAGGGAATGTCTGAGGAAAGCTTTGAGGAG 300
QY 101 SerThrProAsnTyrGlyGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB 301 TCCGTGACACCCCACTCAAGCAGTGTTCATGAGTTCAATGATTAATGACATGATCTT 360
QY 121 GlyLysIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 361 GGGAAATTTGGGAGGTGTACATTACAAAGATCGTTCAAAATAGTCTCTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArgLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
DB 421 TTCAGTGGCTCACTGTGGCTAAATGCAAGAAAGCATGCTGTCAGGTTGATTTTCACA 480
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 481 TTCATGAGACTAAATGTTCCAGACCTCTCCCATTAAGACTAATTAATTATTTGACCA 540
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 541 GGAAGCCCTGAATGAATTAATTAACAAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 201 CysGInGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 601 TGTGAAGATTTGCTGTGATTAAGAGATGTTGATTTGATTTGATTTGATTTGATTT 660
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleGluGlu 240
DB 661 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGTTCTTCGATCATTAATTAAGAA 720
QY 241 LeuProLys 243
DB 721 CTACCAAAA 729

```



```
RESULT 2
ABT33241
ID ABT33241 standard; DNA; 729 BP.
XX
XX ABT33241;
AC
XX
XX
DT 15-MAY-2003 (first entry)
XX
XX Human tumour-related DNA sequence - SEQ ID NO 511.
DE
XX
XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
XX tumour; breast cancer; cancer; immune response stimulation.
XX
XX Homo sapiens.
OS
XX WO200283956-A1.
XX
XX
XX 24-OCT-2002.
XX
XX 15-APR-2002; 2002WO-US012378.
XX
XX 13-APR-2001; 2001US-00834759.
XX 07-DEC-2001; 2001US-00007805.
XX 13-FEB-2002; 2002US-00076622.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC,
XX Mitcham JT, Xu J, Harlocker SL, Heppler WT, Henderson RA, Fanger GR,
XX Vedvyck TS, McNeill PD, Durham M;
XX
XX WPI; 2003-103376/09.
XX
XX New polypeptide and polynucleotide useful for stimulating and/or
XX expanding T cells specific for a tumor protein and treating breast
XX cancer.
XX
XX Example 1; Page 320; 375pp; English.
XX
XX The invention comprises a method of stimulating and/or expanding T cells
XX specific for a tumour protein. The invention further comprises human
XX nucleic acids and proteins that are associated with tumours (e.g. breast
XX cancer). The method and sequences of the invention are useful for
XX stimulating and/or expanding T cells specific for a tumour protein,
XX detecting the presence of cancer, stimulating an immune response in a
XX patient and treating breast cancer. The present DNA sequence represents a
XX human tumour-related DNA sequence
XX
XX
XX Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.29e-104 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-063-734-122 (1-243) x ABT33241 (1-729)
QY 1 MetATGProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 1 ATGCGACCCCGAGGCCCCCGCGCTCCCGACAGCGGCTCGCGCTCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProIleGlyGlnIle 40
DB 61 CTGCTGCACTGCGCGCGCGCTCGACGCGCTCGACATCCCAAGGGAAGCAAGGCG 120
QY 41 GlnLeuArgGlnArgGlnValValAlaPleuIleArgGlyMetCysLeuGlnGlyProAla 60
DB 121 CAGCTCCGCGCAGAGGAGGTGGTGACCTGTATAAGATGCTTACAAAGGCGCAGCA 180
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
```

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DB 181 GGAGTGCCTGCTCGAGAGCGGAGCCCTGGGCGCAATGTTATTCGGGGTACACTGGGATC 240
QY 81 ProGlyArgAspGlyPheIleGlyGlyIleGlyGlyIleGlyGlyIleGlyGlyIle 100
DB 241 CCAGGTCCGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 101 SerTPrpThrProAsnThrIleGlnCysSerIlePheSerSerLeuAsnThrGlyIleAspLeu 120
DB 301 TCTTGACACCCCACTACAGAGAGTGTTCATGAGAGTTCATGATTAATTAAGATTCCTT 360
QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 361 GGGAAAATTGCGGATGTATACATTTACAAAGATGCCCTCAAAATAGTCTTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysCysGlnArgTPrpThr 160
DB 421 TTCAGTGGCTCAGCTTCGGCTAAATGAGAAATGATGATGCTGACGCTTGATTTTCA 480
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 481 TTCAAATGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTAATTAATTTGAGACCA 540
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluIleLeu 200
DB 541 GGAAGCCCTGAAATGATTTCAACATTAATATTCAGACTCTTCTGTGAGAGACTT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPrpValGlyThrCysSerAsp 220
DB 601 TGTGAAGGAATGTTGCTGATTAATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 221 TyrProIleGlyAspAlaSerThrGlyTPrpAsnSerValSerArgIleIleIleGlu 240
DB 661 TACCCAAAGAGAGATGCTTCACTGATGATGATGATGATGATGATGATGATGATGAT 720
QY 241 LeuProIle 243
DB 721 CTACCAAAA 729
RESULT 3
ADL93173
ID ADL93173 standard; cDNA; 729 BP.
XX
XX ADL93173;
AC
XX
XX 20-MAY-2004 (first entry)
XX
XX Human breast cancer-associated polypeptide cDNA #475.
DE
XX
XX gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
XX gene.
XX
XX Homo sapiens.
XX
XX US2003166022-A1.
XX
XX 04-SEP-2003.
XX
XX
XX 15-APR-2002; 2002US-00124805.
XX
XX
XX 28-DEC-1998; 98US-00222575.
XX
XX 02-APR-1998; 98US-00285480.
XX
XX 23-JUN-1999; 99US-00339338.
XX
XX 02-SEP-1999; 99US-00389681.
XX
XX 03-NOV-1999; 99US-00433826.
XX
XX 17-APR-2000; 2000US-00551621.
XX
XX 08-JUN-2000; 2000US-00590751.
XX
XX 22-JUN-2000; 2000US-00604287.
XX
XX 20-JUL-2000; 2000US-00620405.
XX
XX 13-APR-2001; 2001US-00834759.
XX
XX 07-DEC-2001; 2001US-00007805.
XX
XX 13-FEB-2002; 2002US-00076622.
XX
```

PA (CORI-) CORIXA CORP.
 XX
 XX Houghton RL, Sleath PR, Persing DH;
 XX
 DR WPI: 2003-874918/81.
 XX
 XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
 PT treating breast cancer.
 PS
 XX Example 1; SEQ ID NO 511; 294bp; English.
 XX
 CC The invention relates to an isolated breast cancer-associated
 CC polypeptide. The polypeptide may be used for the diagnosis and treatment
 CC of breast cancers. The methods are useful for detecting the presence of a
 CC cancer in a patient and treating a cancer in a patient. The present
 CC sequence represents cDNA encoding a human breast cancer-associated
 CC polypeptide.
 XX
 SO Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.29e-104 Length: 729
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-063-734-122 (1-243) x ADL93173 (1-729)
 QY 1 MetArgProGlnIleProAlaIleSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 1 ATGCGACCCAGGAGCCCGCCGCTCCCGACAGCGCTCGCGCTCTGCTGCTCTG 60
 QY 21 LeuLeuGlnLeuProAlaIleProSerSerAlaSerGlnIleProGlyGlyGlnIleAla 40
 Db 61 CTGCTCAGCTGCGCGCGCGCTGAGACGCTCTGAGATCCCAAGGAGGAGCAAGAGCGG 120
 QY 41 GlnLeuArgGlnArgGluValAlaIlePleuTyraGlnIleMetCysLeuGlnIleProAla 60
 Db 121 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATTAATGAAATGCTTACAGGGCCAGCA 180
 QY 61 GlyValProGlyArgGlnIleSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 80
 Db 181 GAGAGTCCCTGCTGAGACGCGGAGCCCTGAGGAGCAATGTAATCCGAGTACACCTGAGATC 240
 QY 81 ProGlyArgGlnIlePheLeuGlyGlnIleGlyGlnIleGlyGlnIleGlyGlnIle 100
 Db 241 CCAGGTCCGAGATGATTCAGAGAGAGAGAGAGAGATGCTGAGGAGAGAGCTTTGAGAG 300
 QY 101 SerTyrProAsnTyrIleGlnIleCysSerTyrPheSerLeuAsnTyrGlyIleAspLeu 120
 Db 301 TCTCGACACCCACCACTACAGAGAGGTTCATGAGATTCATTAATTAATGAGCATATGATCTT 360
 QY 121 GlyIleIleAlaGluCysThrPheThrIleMetCysSerSerAlaLeuArgValLeu 140
 Db 361 GGGAGAAATTTGGGAGATGATTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgGlnIleGlyGlnIleGlyGlnIle 160
 Db 421 TTTCGTGCTCACTTCGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 161 PheAsnGlyIleAlaGluCysSerGlyProLeuProIleGlnIleIleIleTyrLeuAspGln 180
 Db 481 TTCAATGAGAGTGAATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 181 GlySerProGlnIleMetAsnSerThrIleAsnIleIleAsnIleIleAsnIleIle 200
 Db 541 GGAAGCCCTGAAAGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 QY 201 CysGlnIleGlyIleGlyIleGlyIleValValValValValValValValValValVal 220
 Db 601 TGTCAAGGAATTTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 221 TyrProIleGlyAspAlaSerThrGlyTyrPheAsnValSerArgIleIleIleGlnIle 240
 Db 661 TACCCAAAGAGAGATCTTCTACTGATGAGAAATTCAGTTTCTGCATCATTAATTAAGAGAA 720
 QY 241 LeuProIle 243
 Db 721 CTACCAAAA 729
 RESULT 4
 ABV99144
 ID ABV99144 standard; cDNA, 732 BP.
 AC ABV99144;
 DT 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 4556.
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW Cytostatic; tumour; gene; ss.
 OS Homo sapiens.
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 PF 30-JAN-2002; 2002WO-US002781.
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265682P.
 PR 09-FEB-2001; 2001US-0267588P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 PA (CORI-) CORIXA CORP.
 XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Heppler WT, Jiang Y;
 PI WPI: 2002-627435/67.
 XX P-PSDB: ABP68636.
 DR
 DR
 XX
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 PS
 XX Example 11; SEQ ID NO 4556; 300bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (1) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a) under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridization, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,29e-104 Length: 732
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-063-734-122 (1-243) x ABV99144 (1-732)

QY 1 MetAArgProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeuLeu 20
 DB 1 ATGCGACCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
 QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyGlyGlyGly 40
 DB 61 CTGCTGACACTGCTCCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGGAGG 120
 QY 41 GInLeuArgGInAArgGlyValValAspLeuTyraSerGlyMetCysLeuGInGlyProAla 60
 DB 121 CAGCTCCGCGAGAGGAGGTGTGTGACCTGTATATGATGTGTCTTACAGGCGCAGCA 180
 QY 61 G1yValProG1yAArgAArgGlySerProG1yAlaAsnVal11eProG1yThrProG1yIle 80
 DB 181 GGAGTCTCTGTGTGAGACGGAGACCTCGGGCCCAATGTTATTCGGGTACACTGGGATC 240
 QY 81 ProG1yAArgAArgGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 241 CCAAGTCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 101 SerTrpThrProAsnTyrlsGInGlySerSerTrpSerSerLeuAsnTyrlsGlyIleAspLeu 120
 DB 301 TCTGTGACACCCACACTACAGACAGTGTTCATGAGTTCATTGATTAATGAGCANTGATCTT 360
 QY 121 G1yLyG1eAlaG1uCySerThrPheThrLyMetArgSerAsnSerAlaLeuArgVal1e 140
 DB 361 GGGAAATATGGAGAGTACATTACAAAGATCGTTCAAAATGTCCTTAAAGAGTTTG 420
 QY 141 PheSerGlySerLeuArgLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
 DB 421 TTCAGTGGCTCACTTGGCTTAAATGCAAGATGCTGAGGCTGTGATTTTCA 480
 QY 161 PheAsnG1yAlaG1uCySerGlyProLeuPro11eG1uAla11e11eTyrlsLeuAspGIn 180
 DB 481 TTCATGAGAGCTGATGTTCAAGACCTCTTCCATTGAGCTTAATTTTGGACCA 540
 QY 181 G1ySerProG1uMetAsnSerThr11eAsn11e11eArgThrSerSerValG1uG1yLeu 200
 DB 541 GGAAGCCCTGAAATGAAATTCACATTAATTCATCGCACTTCTGTGAGAGACTT 600
 QY 201 CyG1uG1y11eG1yAlaG1yLeuValAspValAla11eTrpValG1yThrCysSerAArg 220
 DB 601 TGTGAAGGAATGCTGCTGATTAAGAGATGATGATGATGATGATGATGATGATGAT 660
 QY 221 TyrlsProG1yAspAlaSerThrG1yTrpAsnSerValSerArg11e11e11eG1uG1u 240
 DB 661 TACCCAAAGAGATGCTTCTACTGAGATGAGATTCAGTTTCTGCAATCATTTTGAAGAA 720
 QY 241 LeuProGly 243
 DB 721 CTACCAAAA 729

RESULT 5
 ABS64028
 ID ABS64028 standard; cDNA; 732 BP.
 XX
 XX ABS64028;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 XX Human breast tumour polynucleotide #477.
 XX
 XX Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
 KM

vaccine.

XX Homo sapiens.

XX US2002085998-A1.

XX 04-JUL-2002.

XX 13-APR-2001; 2001US-00834759.

XX 28-DEC-1998; 98US-00222575.

XX 02-APR-1999; 99US-00285480.

XX 23-JUN-1999; 99US-00339338.

XX 02-SEP-1999; 99US-00389681.

XX 03-NOV-1999; 99US-00433826.

XX 17-APR-2000; 2000US-00551621.

XX 08-JUN-2000; 2000US-00590751.

XX 22-JUN-2000; 2000US-00604287.

XX 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Dillon DC, Matcham JL, Xu J, Harlocker SL, Hepler WT;

XX Henderson RA;

XX WPI: 2002-635657/68.

XX P-PSDB; ABG78938.

XX Novel breast cancer polynucleotides and polypeptides encoded by the

XX polynucleotides, useful for detecting the presence of breast cancer in a

XX patient, and in pharmaceutical compositions, for treating breast cancer.

XX Claim 1, Page 234; 247pp; English.

XX The invention relates to an isolated breast tumour polynucleotide and the

XX polypeptide it encodes. The polynucleotide and polypeptide are useful for

XX detecting the presence of breast cancer in a patient, and in

XX pharmaceutical compositions for treating breast cancer. The sequences are

XX useful for stimulating an immune response in a patient and can therefore

XX be used in production of vaccines. The sequences are also useful for

XX detecting the presence of a cancer in a patient, by obtaining a

XX biological sample from the patient, contacting the biological sample with

XX a composition of the invention and detecting the amount of polynucleotide

XX that hybridizes to the sample. This sequence represents a human breast

XX tumour polynucleotide of the invention

XX Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 1,29e-104 Length: 732

XX Score: 1301.00 Matches: 243

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX Gaps: 0

XX US-10-063-734-122 (1-243) x ABS64028 (1-732)

QY 1 MetAArgProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeuLeu 20

DB 1 ATGCGACCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60

QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyGlyGlyGly 40

DB 61 CTGCTGACACTGCTCCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGGAGG 120

QY 41 GInLeuArgGInAArgGlyValValAspLeuTyraSerGlyMetCysLeuGInGlyProAla 60

DB 121 CAGCTCCGCGAGAGGAGGTGTGTGACCTGTATATGATGTGTCTTACAGGCGCAGCA 180

QY 61 G1yValProG1yAArgAArgGlySerProG1yAlaAsnVal11eProG1yThrProG1yIle 80

DB 181 GGAGTCTCTGTGTGAGACGGAGACCTCGGGCCCAATGTTATTCGGGTACACTGGGATC 240

Db 721 CTACCAAAA 729
|||||
RESULT 7
ADL93172
ID ADL93172 standard; cDNA; 732 BP.
XX
AC ADL93172;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human breast cancer-associated polypeptide cDNA #474.
XX
KW gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
XX
OS Homo sapiens.
XX
PN US2003166022-A1.
XX
PD 04-SEP-2003.
XX
PF 15-APR-2002; 2002US-00124805.
XX
PR 28-DEC-1998; 98US-00222575.
XX
PR 02-APR-1999; 99US-00285480.
XX
PR 23-JUN-1999; 99US-00339338.
XX
PR 02-SEP-1999; 99US-00388681.
XX
PR 03-NOV-1999; 99US-00433826.
XX
PR 17-APR-2000; 2000US-00551621.
XX
PR 08-JUN-2000; 2000US-00590751.
XX
PR 22-JUN-2000; 2000US-00604287.
XX
PR 20-JUL-2000; 2000US-00620405.
XX
PR 13-APR-2001; 2001US-00834759.
XX
PR 07-DEC-2001; 2001US-00007805.
XX
PR 13-FEB-2002; 2002US-00076622.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RI, Sleath PR, Persing DH;
XX
DR WPI; 2003-874918/81.
XX
DR P-PSDB; ADL93176.
XX
XX
PT An isolated oncogenic polypeptide useful for preventing, diagnosing and
XX
PT treating breast cancer.
XX
XX
PS Example 1; SEQ ID NO 510; 294pp; English.
XX
XX
CC The invention relates to an isolated breast cancer-associated
XX
CC polypeptide. The polypeptide may be used for the diagnosis and treatment
XX
CC of breast cancers. The methods are useful for detecting the presence of a
XX
CC cancer in a patient and treating a cancer in a patient. The present
XX
CC sequence represents cDNA encoding a human breast cancer-associated
XX
CC polypeptide.
XX
SQ Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.29e-104 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-10-063-734-122 (1-243) x ADL93172 (1-732)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 1 ATGGCGACCCCGAGGCGCCCGGCTCCCGCAGCGGCTCCGCTGCTGCTCCG 60
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnLeu 40

Db 61 CTGCTGACAGCTGCCCGCCCGCTGAGCGCTCTGAGATCCCAAGGAGAAAGAAAGCGG 120
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 121 CAGCTCCCGCAGAGGAGGTGTGAGCCGTATTAATGTGAAATGTGCTTACAAAGCCACGA 180
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTyrProGlyIle 80
Db 181 GGAGTGCCTGTCGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTCACCTGGGATC 240
QY 81 ProGlyArgAspGlyPheLeuGlyGlyLeuGlyGlyCysLeuArgGlySerPheGlnGlu 100
Db 241 CCAGTCGGGATGATTTCAAGAGAAAGGAGAAATGCTGAGGAAAGCTTTGAGGAG 300
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
Db 301 TCCTGGACACCCACACTACAGCAGGTTCATGAGTTCATTGAATTAATGGCATTAATCTT 360
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 361 GGAGAAATTCGGAGTGTACATTTCACAAAGATCGCTTCAAAATAGTGTCTTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 421 TTCAGTGGCTCACTTCGGCTAAATGACAAATGATGATGTCAGCGTTGATTTCACA 480
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db 481 TTCAAATGAGCTGAATGTTCAGAGACCTCTCCCATTTGAAGCTATTAATTTGAGCCAA 540
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db 541 GGAAGCCCTGAATATTAATTCACAAATTAATTCATGACATTCCTGCGAAGAGACTT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAsp 220
Db 601 TGTGAAGAAATGTGTGCTGATTAATGATGTGCTATCTGCTATGCGACTTGTTCAGAT 660
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
Db 661 TACCCAAAGAGAGATGCTTCTACTGATGAGATTCAGTTTCGCGATCATTAATGAGAA 720
QY 241 LeuProLys 243
Db 721 CTACCAAAA 729
RESULT 8
ABV99145
ID ABV99145 standard; cDNA; 837 BP.
XX
AC ABV99145;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 4557.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX
KW Cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
XX
PR 31-JAN-2001; 2001US-0265682P.
XX
PR 09-FEB-2001; 2001US-0267568P.
XX
PR 21-MAR-2001; 2001US-0278651P.
XX
PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.

XX
 PA (CORI-) CORIXA CORP.

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX WPI; 2002-627435/67.
 DR P-PSDB; ABP66637.

XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.

XX
 PS Example 11; SEQ ID NO 4557; 300pp + Sequence Listing; English.

XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-
 CC ABP66637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pot_sequences

XX
 SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.53e-104 Length: 837
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x ABV99145 (1-837)

QY 1 MetatgProginglYProAlaIaSerProGlnArgLLeuLeuLeuLeu 20
 DB 106 ATGCGACCCCGAGGCGCCGCGCTCCCGCGAGCGGCTCCGCTGCTCTG 165
 QY 21 LeuLeuGlnLeuProAlaIaSerSerAlaSerGlnLeuProLYsGlnLYsAla 40
 DB 166 CTGCTGAGCTGCGCGCGCGCTGCGAGCGCTCTGAGATCCCGAGGGAACCAAGGCG 225
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTYrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 226 CAGCTCCGCGAGAGGAGGAGTGTGACCTGTATATGAAATGTGTTACAGAGGCGACCA 285
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThProGlyIle 80
 DB 286 GGAAGTGCCTGTGTCAGACGAGGCGCTGGGCGCAATGTTATCCGGGTACACCTGGATC 345
 QY 81 ProGlyArgAspGlyPheLYsGlyGlnLYsGlyValGlyLeuArgGlyLeuSerPheGlyGlu 100
 DB 346 CCAAGTCCGAGATGATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
 QY 101 SerTyrThrProAsnTYrLYsGlnCysSerTyrSerSerLeuAsnTYrGlyIleAspLeu 120
 DB 406 TCCGTGACACCCCACTCAAGCACTGTTCATGAGGATTCATTGAAATTATGGCATAGATCTT 465
 QY 121 GlyValIleAlaGlyCysThrPheThrLYsMetArgSerAsnSerAlaLeuArgValLeu 140

DB 466 GGGAAATATGCGAGATGTACATTTACAAAGATGCGTTCAATAGTGTCTAAGATTG 525
 QY 141 PheSerGlySerLeuArgLeuLYsCysArgAsnAlaCysCysGlnArgTYrPheThr 160
 DB 526 TTCAGTGGCTTCACTTGGCTTAAAGCAAGATCATGCTGTCAGCGCTTGATTTTACA 585
 QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTYrLeuAspGln 180
 DB 586 TTCATGAGAGTGTATGTTACAGACCTTCCATTACATTAATTTATTTGGACCA 645
 QY 181 GlySerProGlyMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200
 DB 646 GGAAGCCCTGAAAGATTAATCAACATTAATTCATGCACTTCTTGAGAAAGACTT 705
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleThrValGlyThrCysSerAsp 220
 DB 706 TGTGAAGAAATTTGGTGGATTTAGTGAATGTTGCTACTGCGGTGCACTGTTGAGAT 765
 QY 221 TyrProLYsGlyAspAlaSerThrGlyTYrPAsnSerValSerArgIleIleIleGlyGlu 240
 DB 766 TACCAAAAGAGATGCTTACTAGATGATGAAATTCAGTTCTCGCATCATTTAGAGA 825
 QY 241 LeuProLYs 243
 DB 826 CTACCAAAA 834

RESULT 9
 ID ABS64030 standard; CDNA; 837 BP.
 XX ABS64030;
 AC 15-NOV-2002 (first entry)
 XX
 DT Human breast tumour polynucleotide #479.
 XX
 DE Human, breast tumour protein; gene; ss; breast cancer; cytostatic;
 XX
 KW Human vaccine.
 XX
 OS Homo sapiens.
 XX
 EN US2002085998-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 13-APR-2001; 2001US-00834759.
 XX
 PR 28-DEC-1998; 98US-00222575.
 PR 02-APR-1999; 99US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 PI Henderson RA;
 XX
 DR WPI; 2002-635657/68.
 DR P-PSDB; ABG78939.
 XX
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 PS Claim 1, Page 234-235; 247pp; English.
 XX
 CC The invention relates to an isolated breast tumour polynucleotide and the

CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention

XX Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 1,53e-104 | length: | 837 |
|------------------------|-----------|---------------|-----|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ABS64030 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 DB 106 ATGCGACCCGAGGGCCCGCCGCCGACGGGCTCCGGGCTCCGCTGCTCTCTG 165
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnLeuAla 40
 DB 166 CTGCTTCAGTGCCTCCGCGCTCGAGGCGCTCTGAGTCTCCCAAGGGGAAAGCGCG 225
 QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 226 CAGCTTCGGGAGGAGGAGGTGTGACCTTATATGATGATGCTTACAGGGCCAGCA 285
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
 DB 286 GAGAGTCCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 345
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 346 CCGAGTCTGGGATGATTCAAAGAGAAAGGGGAGATGTCTGAGGGAACCTTTGAGGAG 405
 QY 101 SerTrpThrProAsnTyrIleValGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 406 TCTTGGACACCCACATCAAGACAGTGTTCATGAGTTCATTGATTAATGACATAGATCTT 465
 QY 121 GlyLeuIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 466 GCGAAATATGCGAGTGTACATTACAAAGATCGTTCAAAATGTGCTCAAGAGTTTG 525
 QY 141 PheSerGlySerLeuArgLeuLeuValGlyValGlyValGlyValGlyValGlyVal 160
 DB 526 TTGAGTGGCTCAGCTTGGCTAAATGAGAAATGATGCTGTCAGCGCTTGATTTTCA 585
 QY 161 PheAsnGlyValAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
 DB 586 TTCAATGAGACTAAATGTTGAGACCTCTTCCCATTTGAAACCTAAATTAATTTGAGCAA 645
 QY 181 GlySerProGlnLeuMetArgSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
 DB 646 GGAAGCCCTGAATGATTCACACATTAATTCATGCGACTTCTCTGAGAGAGACTT 705
 QY 201 CysGluGlyTyrLeuAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
 DB 706 TGTGAAGGATTTGTCTGTGATGAGATGTTGCTATCGGCTTGCGACTTGTTCAGAT 765
 QY 221 TyrProGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
 DB 766 TACCCAAAGAGATGCTTCTACTGAGTGAATTCAGTTTCTGCACTAATTAAGAGAA 825
 QY 241 LeuProGly 243
 |||||

DB 826 CTACCAAAA 834

RESULT 10

ABS64031
 ID ABS64031 standard; cDNA, 837 BP.

XX ABS64031;

DT 15-NOV-2002 (first entry)

DE Human breast tumour polynucleotide #480.

KW Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
 KM vaccine.

OS Homo sapiens.

PN US2002085998-A1.

PD 04-JUL-2002.

PF 13-APR-2001; 2001US-00834759.

PR 28-DEC-1998; 98US-00222575.

PR 02-APR-1999; 99US-00285480.

PR 23-JUN-1999; 99US-00339338.

PR 02-SEP-1999; 99US-00389681.

PR 03-NOV-1999; 99US-00433826.

PR 17-APR-2000; 2000US-00551621.

PR 08-JUN-2000; 2000US-00590751.

PR 22-JUL-2000; 2000US-00604287.

PR 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 PI Henderson RA;

XX WPI; 2002-635657/68.

XX P-PSDB; ABG78939.

XX Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.

XX Claim 1; Page 235; 247pp; English.

XX The invention relates to an isolated breast tumour polynucleotide and the
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention

XX Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 1,53e-104 | length: | 837 |
|------------------------|-----------|---------------|-----|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ABS64031 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 |||||

Db 106 ATCCGACCCGAGCCGCCGCCCTCCCGCAGCGGCTCCGGGCTCTCTGCTGCTCCG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVala 40
Db 166 CTGCTGACAGCTGCCGCCGCCCTCGAGCGCTCTGAGATCCCGAGGAGGAGGAGGCG 225
QY 41 GlnLeuArgGlnArgGluValaValaLeuLeuTyraanglyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGCGCAGAGGAGGTGTGAGCTGTATATGAAATGTGCTTCAAGGGGCGAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaSerValLeuProGlyThrProGlyTle 80
Db 286 GAGAGTCTGCTGCGAGAGCGAGGAGCCCTGGGCCCAATGTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 346 CCAGGTCCGAGTGTGATTCAGAAAGAGAAAGGGGGAATCTCGAGGAAAGCTTTGAGAGG 405
QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsLeu 120
Db 406 TCCGTGACACCCCACTACAGACAGGTTCATGAGGTTCATTTGAATTAATGCGATGATCTT 465
QY 121 GlyValleuAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValleu 140
Db 466 GGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAAATGATGCTTAAGAGTTTG 525
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyrrPheThr 160
Db 526 TTCAGTGTCTACTTCGGCTAAATGCAAGAAATGCAATGCTGCTGCTGATTTTCA 585
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProGlyLeuAlaLeuLeuLeuAspGln 180
Db 586 TTCATGTAGACTGATGTTCAGGACCTTCCTCCATTAACCTTAATTAATTTGACCA 645
QY 181 GlySerProGlyMetAsnSerThrTleAsnIleHisArgThrSerSerValGlyGlyLeu 200
Db 646 GGAAGCCCTGAAATGATTCACAAATTAATTAATTCATGACCTTCTGCGAAGAGACTT 705
QY 201 CysGlyGlyTleGlyAlaGlyLeuValAspValAlaIleCysValGlyThrCysSerAsp 220
Db 706 TGTGAAGGAAATGTGCTGATTAATGATGATTTGCTATCTGGGTTGGCACTGTTCA 765
QY 221 TyrProGlyGlyAspAlaSerThrGlyTTPAsnSerValSerArgTleIleGlnGlu 240
Db 766 TACCCCAAGAGATGCTTCTACTGATGATGAATTCAGTTTTCGACATTAATTTGAGAA 825
QY 241 LeuProLys 243
Db 826 CTACCAAAA 834

RESULT 11
ABT33242
ID ABT33242 standard; DNA; 837 BP.
XX
AC ABT33242;
XX
DT 15-MAY-2003 (first entry)
XX
DB Human tumour-related DNA sequence - SEQ ID No 512.
XX
KW Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
XX
OS tumour; breast cancer; cancer; immune response stimulation.
XX
XX Homo sapiens.
XX
XX W0200283956-A1.
XX
XX 24-OCT-2002.
XX
XX 15-APR-2002; 2002WO-US012378.
XX
XX 13-APR-2001; 2001US-00834759.
XX
XX 07-DEC-2001; 2001US-00007805.
PR

PR 13-FEB-2002; 2002US-00076622.
XX
XX (CORI-) CORIXA CORP.
XX
PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC,
PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR,
PI Vedvick TS, McNeill PD, Durham M,
XX
XX WPI; 2003-103376/09.
XX
XX New polypeptide and polynucleotide useful for stimulating and/or
XX expanding T cells specific for a tumor protein and treating breast
XX cancer.
XX
XX Example 1; Page 320; 375pp; English.
XX
XX The invention comprises a method of stimulating and/or expanding T cells
XX specific for a tumor protein. The invention further comprises human
XX nucleic acids and proteins that are associated with tumors (e.g. breast
XX cancer). The method and sequences of the invention are useful for
XX stimulating and/or expanding T cells specific for a tumor protein,
XX detecting the presence of cancer, stimulating an immune response in a
XX patient and treating breast cancer. The present DNA sequence represents a
XX human tumour-related DNA sequence
XX
SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,53e-104 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
XX
US-10-063-734-122 (1-243) x ABT33242 (1-837)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
Db 106 ATCCGACCCGAGGCCCCGCCGCCCTCCCGCAGCGGCTCCGGGCTCTCTGCTGCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVala 40
Db 166 CTGCTGACAGCTGCCGCCGCCCTCGAGCGCTCTGAGATCCCGAGGAGGAGGAGGCG 225
QY 41 GlnLeuArgGlnArgGluValaValaLeuLeuTyraanglyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGCGCAGAGGAGGTGTGAGCTGTATATGAAATGTGCTTCAAGGGGCGAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaSerValLeuProGlyThrProGlyTle 80
Db 286 GAGAGTCTGCTGCGAGAGCGAGGAGCCCTGGGCCCAATGTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 346 CCAGGTCCGAGTGTGATTCAGAAAGAGAAAGGGGGAATCTCGAGGAAAGCTTTGAGAGG 405
QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsLeu 120
Db 406 TCCGTGACACCCCACTACAGACAGGTTCATGAGGTTCATTTGAATTAATGCGATGATCTT 465
QY 121 GlyValleuAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValleu 140
Db 466 GGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAAATGATGCTTAAGAGTTTG 525
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyrrPheThr 160
Db 526 TTCAGTGTCTACTTCGGCTAAATGCAAGAAATGCAATGCTGCTGCTGATTTTCA 585
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProGlyLeuAlaLeuLeuLeuAspGln 180
Db 586 TTCATGTAGACTGATGTTCAGGACCTTCCCTTAACCTTAATTAATTTGACCA 645

XX 15-APR-2002; 2002US-00124805.
PF 28-DEC-1998; 98US-00222575.
XX 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
PR 13-APR-2001; 2001US-00834759.
PR 07-DEC-2001; 2001US-00007805.
PR 13-FEB-2002; 2002US-00076622.
XX (CORI-) CORIXA CORP.
XX Houghton RL, Sleath PR, Persing DH;
PI WPI, 2003-874918/81.
XX P-PSDB; ADL93177.
DR
XX
XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
PT treating breast cancer.
XX
PS Example 1; SEQ ID NO 512; 294pp; English.
XX
CC The invention relates to an isolated breast cancer-associated
CC polypeptide. The polypeptide may be used for the diagnosis and treatment
CC of breast cancers. The methods are useful for detecting the presence of a
CC cancer in a patient and treating a cancer in a patient. The present
CC sequence represents cDNA encoding a human breast cancer-associated
CC polypeptide.
XX
SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1 53e-104 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-10-063-734-122 (1-243) x ADL93174 (1-837)
QY 1 MetAAGPProGInGlyProAlaAlaSerProGInArGLeuArGlyLeuLeuLeuLeu 20
Db 106 ATGCGACCCCAAGGCGCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTCTGCTG 165
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGInLeuAla 40
Db 166 CTGCTGCGAGCTGCGCGCGCTGAGCGCTCTGAGATCCCAAGGAGCAAAAGCGG 225
QY 41 GInLeuArGInArGInValValAspLeuTyraAnglyMetCysLeuGInGlyProAla 60
Db 226 CAGCTCCCGCAGAGGAGGAGTGTGACCTGATATATGAAATGCTTCAAGGGCCACA 285
QY 61 GInValPProGInArGAspGlySerProGlyAlaValAlaProGlyThrProGlyTle 80
Db 286 GGAAGTCTGTGTCAGACGAGGAGCCCTGGGCGCATGTTATCCGGGTACACCTGGGATC 345
QY 81 ProGlyArGAspGlyPheLeuGlyGluValGlyGluCysLeuArGInGlySerPheGluGlu 100
Db 346 CCAAGTGGGAGTGAATCAAGAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGAGAG 405
QY 101 SerTrpThrProAlaTrpTyrLeuGInCysSerTrpSerSerLeuAlaTrpTyrTleAspLeu 120
Db 406 TCCCTGACACCCCACTCAAGACAGTGTTCATGAGTTCATTTGATATATGATGATCTT 465
QY 121 GInValTleAlaGluCysThrPheThrTlyMetCysSerAlaLeuArGValLeu 140

Db 466 GGGAAATTCGAGAGTGTACATTTACAAAGATGCGCTTCAATAGNGCTTAAGATTG 525
QY 141 PheSerGlySerLeuArGLeuLeuYsCysArgSerAlaCysCysGInaGTrpTyrPheThr 160
Db 526 TTCAGTGGCTTCACTTCGGCTTAATGACAAATGACAGATGCTGTGAGCGTTGGTATTCACA 585
QY 161 PheAnglyAlaGluCysSerGlyProLeuProGInGluAlaTleTyrLeuAspGIn 180
Db 586 TTCATGAGAGTGAATGTTACAGACCTTCCATTTGAGCTATATTTATTTGACCA 645
QY 181 GlySerProGluMetAspSerThrTleAsnTleHisArgThrSerSerValGluGlyLeu 200
Db 646 GGAAGCCCTGAATATTAATCAACATTAATTCATGACACTTCTCTGTGGAAGACCTT 705
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaTleTrpValGlyThrCysSerAsp 220
Db 706 TGTGAAGAGATGTGTGCTGAGATTAGTGTGATCTTCTGAGTTGACACTTGTGAGAT 765
QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGIn 240
Db 766 TACCCAAAGAGAGATGCTTCTTACAGATGAGATTCAGTTCTCGCATTTATTGAAGA 825
QY 241 LeuProLys 243
Db 826 CTACCAAAA 834
RESULT 14
ADL93175
ID ADL93175 standard; cDNA; 837 BP.
XX
AC ADL93175;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human breast cancer-associated polypeptide cDNA #477.
XX
KW gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
KW gene.
XX
OS Homo sapiens.
XX
PN US2003166022-A1.
XX
PD 04-SEP-2003.
XX
PF 15-APR-2002; 2002US-00124805.
XX
PR 28-DEC-1998; 98US-00222575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
PR 13-APR-2001; 2001US-00834759.
PR 07-DEC-2001; 2001US-00007805.
PR 13-FEB-2002; 2002US-00076622.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Sleath PR, Persing DH;
XX
DR WPI, 2003-874918/81.
XX
XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
PT treating breast cancer.
XX
PS Example 1; SEQ ID NO 513; 294pp; English.
XX
CC The invention relates to an isolated breast cancer-associated
CC polypeptide. The polypeptide may be used for the diagnosis and treatment

CC of breast cancers. The methods are useful for detecting the presence of a
CC cancer in a patient and treating a cancer in a patient. The present
CC sequence represents cDNA encoding a human breast cancer-associated
CC polypeptide.

XX SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 1 53e-104 | Length: | 837 |
|------------------------|-----------|---------------|-----|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 11 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ADB93175 (1-837)

```

QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGCGACCCGAGGCGCCGCGCTCCGCGACGGGCTCCGCGCTCTGCTGCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLysAla 40
DB 166 CTGCTGCACGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGCAAAAGGCG 225
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGGAGAGGAGGAGGTGTGACCTGTATTAAGAAATGTCTTACAGGGCCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyLys 80
DB 286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATTTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100
DB 346 CCGAGTCGGGATGATTCAGAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTGTAGGAG 405
QY 101 SerTrpThrProAsnTrpLysGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120
DB 406 TCTGTGACACCCCACTACACAGCTGTCTGAGAGTTCATTGAATTAATGCGATGATCTT 465
QY 121 GlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATATTCGAGAGTGTACATTACAAAGATCCGTTCAATATGTCTCTMAAGATTTC 525
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpLysPheThr 160
DB 526 TTCAGTGGCTCACTTCGGCTAAATATGACAAATGATGATGCTGACGCTGTGATTCACA 585
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 586 TTCAAATGAGAGCTGAATGTTCAGAGACCTCTCCATTTGAACCTTAAATTTATTTGAGCAA 645
QY 181 GlySerProGlnLysSerAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 646 GGAAGCCCTGGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 705
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyLysSerAsp 220
DB 706 TGTGAAGGAATGTGTCTGATTAAGATGTTGCTATCTGAGGTGTGCACTTGTTCAGAT 765
QY 221 TyrProLysGlyAspAlaSerThrArgLysPheAsnSerValSerArgLysIleIleGlnGlu 240
DB 766 TACCCCAAAAGAAATCTTCTACTGATGATGAAATTCAGTTTCTGCAATTAATTAAGAA 825
QY 241 LeuProLys 243
DB 826 CTACCAAAA 834

```

RESULT 15
ADB90997
ID ADB90997 standard; cDNA; 1256 BP.
XX

AC ADB90997;
XX
DT 04-DEC-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1550 cDNA.

KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KM affinity purification; secreted and transmembrane protein.

XX Homo sapiens.

XX US2003083473-A1.

XX 01-MAY-2003.

XX 03-MAY-2002; 2002US-00063595.

XX 06-DEC-2001; 2001US-00006867.

XX (GETH) GENENTECH INC.

XX Eaton DJ, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-786922/74.

XX P-PSDB; ADB90998.

XX New antibody that binds a secreted and transmembrane polypeptide (PRO)
XX for treating cancer and for diagnostic assays and affinity purification
XX of PRO.

XX Disclosure; Fig 121; 408pp; English.

XX The invention describes an antibody that specifically binds to a PRO
XX polypeptide having a fully defined amino acid sequence given in the
XX specification. The antibody is useful in identifying PRO polypeptides
XX useful for various industrial applications, including pharmaceuticals,
XX diagnostic, biosensors and bioreactors. The antibody is also used for
XX affinity purification of PRO polypeptides from recombinant cell culture
XX or natural sources. The antibody, PRO polypeptide, or its agonists or
XX antagonists, may be used for preparing a medicament for diagnosing or
XX treating a condition responsive to the antibody, PRO polypeptide, or its
XX agonists or antagonists. This sequence encodes a novel human secreted and
XX transmembrane PRO polypeptide.

XX SQ Sequence 1256 BP; 324 A; 264 C; 299 G; 369 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 2 54e-104 | Length: | 1256 |
|------------------------|-----------|---------------|------|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ADB90997 (1-1256)

```

QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCGAGGCGCCGCGCTCCGCGACGGGCTCCGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLysAla 40
DB 198 CTGCTGCACGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGTGTGACCTGTATTAATGAAATGTCTTACAGGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyLys 80
DB 318 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATTTATTCGGGTACACCTGGGATC 377

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| | | |
|----|--------------|---------------|
| PR | 10-SEP-1998; | 98US-0039812P |
| PR | 10-SEP-1998; | 98US-0039815P |
| PR | 10-SEP-1998; | 98US-0039816P |
| PR | 15-SEP-1998; | 98US-0100385P |
| PR | 15-SEP-1998; | 98US-0100388P |
| PR | 15-SEP-1998; | 98US-0100390P |
| PR | 16-SEP-1998; | 98US-0100540P |
| PR | 16-SEP-1998; | 98US-0100617P |
| PR | 16-SEP-1998; | 98US-0100621P |
| PR | 16-SEP-1998; | 98US-0100622P |
| PR | 16-SEP-1998; | 98US-0100643P |
| PR | 17-SEP-1998; | 98US-0100643P |
| PR | 17-SEP-1998; | 98US-0100644P |
| PR | 17-SEP-1998; | 98US-0100710P |
| PR | 17-SEP-1998; | 98US-0100711P |
| PR | 17-SEP-1998; | 98US-0100919P |
| PR | 18-SEP-1998; | 98US-0100930P |
| PR | 18-SEP-1998; | 98US-0100948P |
| PR | 18-SEP-1998; | 98US-0100949P |
| PR | 18-SEP-1998; | 98US-0101014P |
| PR | 18-SEP-1998; | 98US-0101068P |
| PR | 22-SEP-1998; | 98US-0101271P |
| PR | 22-SEP-1998; | 98US-0101272P |
| PR | 22-SEP-1998; | 98US-0101471P |
| PR | 22-SEP-1998; | 98US-0101472P |
| PR | 22-SEP-1998; | 98US-0101474P |
| PR | 22-SEP-1998; | 98US-0101475P |
| PR | 22-SEP-1998; | 98US-0101476P |
| PR | 22-SEP-1998; | 98US-0101477P |
| PR | 22-SEP-1998; | 98US-0101479P |
| PR | 24-SEP-1998; | 98US-0101736P |
| PR | 24-SEP-1998; | 98US-0101741P |
| PR | 24-SEP-1998; | 98US-0101743P |
| PR | 24-SEP-1998; | 98US-0101915P |
| PR | 24-SEP-1998; | 98US-0101916P |
| PR | 29-SEP-1998; | 98US-0102240P |
| PR | 29-SEP-1998; | 98US-0102247P |
| PR | 29-SEP-1998; | 98US-0102307P |
| PR | 29-SEP-1998; | 98US-0102330P |
| PR | 29-SEP-1998; | 98US-0102331P |
| PR | 30-SEP-1998; | 98US-0102484P |
| PR | 30-SEP-1998; | 98US-0102487P |
| PR | 30-SEP-1998; | 98US-0102570P |
| PR | 30-SEP-1998; | 98US-0102571P |
| PR | 01-OCT-1998; | 98US-0102644P |
| PR | 01-OCT-1998; | 98US-0102647P |
| PR | 02-OCT-1998; | 98US-0102655P |
| PR | 06-OCT-1998; | 98US-0103258P |
| PR | 07-OCT-1998; | 98US-0103314P |
| PR | 07-OCT-1998; | 98US-0103315P |
| PR | 07-OCT-1998; | 98US-0103328P |
| PR | 07-OCT-1998; | 98US-0103355P |
| PR | 07-OCT-1998; | 98US-0103366P |
| PR | 08-OCT-1998; | 98US-0103401P |
| PR | 08-OCT-1998; | 98US-0103633P |
| PR | 08-OCT-1998; | 98US-0103678P |
| PR | 08-OCT-1998; | 98US-0103679P |
| PR | 14-OCT-1998; | 98US-0103711P |
| PR | 14-OCT-1998; | 98US-0104257P |
| PR | 20-OCT-1998; | 98US-0104967P |
| PR | 20-OCT-1998; | 98US-0105000P |
| PR | 21-OCT-1998; | 98US-0105104P |
| PR | 22-OCT-1998; | 98US-0105159P |
| PR | 22-OCT-1998; | 98US-0105266P |
| PR | 26-OCT-1998; | 98US-0105633P |
| PR | 27-OCT-1998; | 98US-0105634P |
| PR | 27-OCT-1998; | 98US-0105807P |
| PR | 27-OCT-1998; | 98US-0105817P |
| PR | 27-OCT-1998; | 98US-0106082P |
| PR | 27-OCT-1998; | 98US-0106082P |

PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108825P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PA (GETH) GENENTECH INC.

XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
 PI WPI, 2000-237871/20.
 XX P-PSDB; AAY99462.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 2; Fig 245; 773bp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention

XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

XX Alignment Scores:
 Pred. No.: 2 55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-063-734-122 (1-243) x AAA37144 (1-1257)

QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 DB 138 ATCGACACCCAGGCGCCCGCTCCCGCACGCGCTCGGCGCTCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProLeuGlyLeuGlnLeu 40
 DB CTGCTGCACTGCTCCCGCCCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGG 257
 QY 41 GlnLeuArgGlnArgGluValAlaIaIaSerLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
 DB CAGCTCCGGCAGAGGAGGTGTGTGACCTGTATATGGAATGTGCTTACAAAGGCCACAGA 317
 QY 61 GlyValProGlnValArgAspGlySerProGlyAlaIaIaIaIaIaIaIaIaIaIaIaIa 80
 DB GGAGTGCCTGCTCGAGACGCGGAGCCCTGGGCGCAATGTATTTCCGGGTACACCTGGAGTC 377
 QY 81 ProGlyArgAspGlyPheIleGlyGlyLeuGlyGlyCysLeuArgGlyIleSerPheGlnGlu 100
 DB CAGGTCCGGAGTGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 437
 QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
 DB TCCTGGACACCCCACTACACAGCAGTGTTCATGTAGTTCATTAATTAATGACATGATCTT 497
 QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerSerAlaIaIaIaIaIaIaIa 140
 DB GGGAATTTGCGAGATGTACATTTACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGG 557
 QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysCysGlnArgTrpThrPheThr 160
 DB TTCAGTGGCTTCACTTCGCTTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 617
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlaAspGln 180
 DB TTCATATGAGCTGAGATGTTCAAGACCTCTCCATTTGAAGCTATATTTATTTGACCA 677
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIleIle 200
 DB GGAAGCCCTGAATGATTCACCAATTAATTCATTCGACCTTCTCTGTGAAGACCTT 737
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
 DB TGTGAAGGATTTGTGCTGGATTTAGTGAATGTCTATTCGAGTTGGACCTTGTTCAGAT 797
 QY 221 TyrProLeuGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGln 240
 DB TACCAAAAGAGAGATGCTTCACTGAGATGATTAAGTTCTCGCATCATTTATTTGAAGA 857
 QY 241 LeuProLeu 243
 DB 858 CTACCAAAA 866

RESULT 17
 AAF54507
 ID AAF54507 standard; DNA; 1257 BP.
 XX AAF54507;
 AC AAF54507;
 XX 02-APR-2001 (first entry)
 DT
 XX Probe #60 used in the identification of proteins.
 DE
 XX Secreted; transmembrane; gene therapy; ss.
 KW
 XX Unidentified.
 OS
 XX WO200078961-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 18-FEB-2000; 2000KO-US004342.
 PF
 XX 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.

03-MAY-2000; 2000US-0201516P.
17-MAY-2000; 2000WO ITC01370E

PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX P-PSDB; AAU29206.
XX WPI; 2001-602746/68.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 365; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumor in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumor necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumors and also
CC susceptibility to tumor development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x AAS46107 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCGACCCCGAGGAGCCCGCGCTCCCGACGGGTCCGCGCCCTCCGCTGCTC 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGly 40
Db 198 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAGAAAAGGGG 257
QY 41 GlnLeuArgGlnArgGluValValAlaPLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGGAGGAGGTGGGACCTGATTAAGGATGCTTACCAAGGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGAGCTCGTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTCGGGTACCACTGGGAGAT 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGGGATGATTCAAAGAGAAAGGGGAATGTCTGAGGGAAGCTTTGAGAG 437

QY 101 SerTrpThrProAsnTyrGlyGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCTGTGACACCCCACTACAGACAGTGTTCATGAGATTCATTGAATATGACATGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCCGAGTGTCAATTACAAAGATGCCGTTCAAAATAGTCTCTAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTrpPheThr 160
Db 558 TTCAGTGGCTCACTTCGCTAAAGATGACAAATGATGATGCTGCAGGTTGGATTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGCTGATGATGTTCAAGACCTCTTCCCATTTGAAGCTAATATTTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATATGATTCACAAATTAATTCATGCGACTTCTTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAlaPLeuAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGGTGGCTGTGATTAAGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAGAGATGCTTCTACTGGATGAATTCAGTTTCGCACTATTAATGAAGA 857
QY 241 LeuProGly 243
Db 858 CTACCAAA 866

RESULT 19
AAF92118
ID AAF92118 standard; cDNA; 1257 BP.
XX
AC AAF92118;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1550 cDNA.
XX
XX Human; PRO protein; mapping; se.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000MO-US023328.
XX
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US020190.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000MO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000MO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
XX (GETH) GENENTECH INC.
XX
PI Saton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,

201 CysGIuGIYIleGIyAlaGIyLeuValAspValAlaIleTrrValGIvThrCvsSerAsn 220

10-SEP-1990; 98US-0099815P.
16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US021252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
(GETH) GENENTECH INC.
Eaton Df, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
WPI: 2002-731348/79.
P-PsDB; ABG95911.

DR New isolated secreted and transmembrane PRO polypeptide useful for
modulating biological activity of a cell, or for treating sports-related
joint problems, osteoarthritis or rheumatoid arthritis.

PS Claim 2, Fig 121, 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
XX polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,

CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridization probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention

XX SQ Sequence 1257 BP, 324 A, 264 C, 299 G, 370 T, 0 U, 0 Other;

Alignment Scores:

| Pred. No.: | 2,55e-104 | Length: | 1257 |
|------------------------|-----------|---------------|------|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ABS74438 (1-1257)

QY 1 MetatgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCAAGGCGCCGCCCTCCCGCAGCGGCTCCGCGCTCCTGCTCCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyValAla 40
DB 198 CTGCTGACGCTCCCGCGCGCTGAGCGCTTGAAGATCCCAAGGAGAAAGAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlyValAlaAspLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAAGGAGGAGTGTGACCTGTATATGAAATGCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAAGTCTGCTGACAGACGAGAGCCCTGGGCGCAATGTATTCCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlyValGlyValGlyValGlyValGlyVal 100
DB 378 CCAAGTCCGGAATGATTCAAAGAGAAAGGAGAAAGTGTAGAGGAAAGCTTTGAGAG 437
QY 101 SerTTPThProAsnTyrlsGlnCysSerTTPSerSerLeuAsnTyrlsIleAspLeu 120
DB 438 TCTTGACACCCCACTACAGACAGTTCATGAGTTCATTGAATTATGCAATGATCTT 497
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAAGAAATGCGAGAGTGCATTTCAAAGAGCGCTTCAAAATAGTCTTAAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuTyrlsCysArgAsnAlaCysCysGlnArgTrpTrpPheThr 160
DB 558 TTCAGTGGCTCACTTCGCTGTAAGAAATGCAATGATGTCAGCGTGTGATTTTCAACA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsAspGln 180
DB 618 TTCATGAGCTGATGATTTCAAGACCTCTCCCATTTGAAGCATATATTTATTTGACCA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleIleArgThrSerSerValGlnGlyLeu 200
DB 678 GGAAGCCCTGAATGATTAATCAATTAATTAATTCATTCGACATTCCTTGTGAGAGACTT 737

Db 558 TTCAGTGGCTCACTTGGCTAAATGACAAATGATGCTGTCAGCGTGGTATTTCACA 617
QY 161 PheAsnGlyValAglyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCATTGAGCTATTAATTTATTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGGAATGATTCACATTAATTAATTCATCGACCTCTCTGTGGAGACATT 737
QY 201 CysGluGlyIleGlyValAglyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCTGCGGTGGCACTGTTCAGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAGAGATCTTCTACTGATGATGGAATTCAGTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProGly 243
Db 858 CTACCAAA 866
RESULT 22
AAD32717
ID AAD32717 standard; cDNA; 1257 BP.
XX
AC AAD32717;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human tumour-associated antigenic target-170 (TAT170) cDNA.
XX
KW Human; tumour-associated antigenic target-170; TAT170; cyclostatic;
KW gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 138..869
FT FT /*tag= a
FT FT /product= "Human TAT170 protein"
FT sig_peptide 138..227
FT FT /*tag= b
FT mat_peptide 228..866
FT FT /*tag= C
FT FT /product= "Mature TAT170 protein"
XX
PN WO200216602-A2.
XX
PD 28-FEB-2002.
XX
PF 23-AUG-2001; 2001WO-US026626.
XX
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US036378.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GENTECH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Polakis P;
PI Williams PM, Wood WI, Wu TD, Zhang Z;
XX
XX WPI: 2002-292065/33.
XX P-PSDB; AAE20462.
XX
PT New antibodies that bind tumor-associated antigenic target (TAT)
PT polypeptides, useful for treating and diagnosing tumor (e.g. breast,

PT lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle, pigs,
PT goats, rabbits or humans.
XX
PS Claim 1; Fig 2; 124pp; English.
XX
CC The present invention relates to an isolated antibody that binds to tumor
CC -associated antigenic target (TAT) polypeptide. The antibody is used for
CC treating and diagnosing tumors (e.g. breast, lung, liver or stomach
CC tumors) in mammals, e.g. dogs, cats, cattle, horses, sheep, pigs, goats,
CC rabbits, or preferably humans. The antibody may also be used in antibody-
CC dependent enzyme mediated prodrug therapy (ADEPT). The antibody is also
CC useful for the therapeutic treatment or for the diagnostic detection of
CC cancer. TAT cDNA is useful in gene therapy. The present sequence is human
CC TAT170 cDNA designated DNA76393-1664
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x AAD32717 (1-1257)

QY 1 MetArgProGlnGlyProAlaAspProGlnArgLeuLeuLeuLeu 20
Db 138 ATGCGACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGCTCTGCTGCTCCG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyValGlnValAla 40
Db 198 CTGCTGACCTGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCGG 257
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGACAGAGGAGGTGTGAGCTGTATATGAAATGTGCTTACAGGCGCAGCA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAAGTCCCTGCTCGAGACCGGAGCCCTGGGCGCAATGTATATCCGGGTACCTTGAGATC 377
QY 81 ProGlyArgAspGlyPheIleGlyGlnValGlnCysLeuArgGlnSerPheGlnGln 100
Db 378 CAGGTCGAGATGATTCAGAGCAAGAAAGGGGAAATGCTTGAAGGAACTTTGAGAG 437
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCCTGACACCCCACTACAGACAGGTGTCATGAGTTCAATTATGATGATGATGATCTT 497
QY 121 GlyIleGlyIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GCGAAATATGCGAGGTGTCATTTCAAAAGAGCGCTTCAATATGCTCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysCysGlnArgThrPheThr 160
Db 558 TTCAGTGGCTCACTTGGCTAAATGACAAATGATGCTGTCAGCGTGGTATTTCACA 617
QY 161 PheAsnGlyValAglyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCATTGAGCTATTAATTTATTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGGAATGATTCACATTAATTAATTCATCGACCTCTCTGTGGAGACATT 737
QY 201 CysGluGlyIleGlyValAglyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCTGCGGTGGCACTGTTCAGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240

Db 798 TACCAAGAGATCTTCTACTGATGATTCATTCGATCATTTATGAGAA 857
 QY 241 LeuProlys 243
 Db 858 CTACCAAAA 866
 RESULT 23
 ABL95683
 ID ABL95683 standard; cDNA, 1257 BP.
 AC ABL95683;
 DT 19-JUL-2002 (first entry)
 DE Human angiogenesis related cDNA PRO1550 SEQ ID NO: 245.
 KW Human; angiogenesis; PRO protein; cardiovascularization; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytosaratic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic; gene; ss.
 OS Homo sapiens.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PF 09-JUL-2001; 2001WO-US021735.
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 28-JUL-2000; 2000US-0220664P.
 XX 02-AUG-2000; 2000US-0222695P.
 XX 17-AUG-2000; 2000US-0064365P.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 07-SEP-2000; 2000US-0230978P.
 XX 18-SEP-2000; 2000US-0066410.
 XX 24-OCT-2000; 2000US-0242922P.
 XX 08-NOV-2000; 2000US-0070323P.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 22-JAN-2001; 2001US-0076760P.
 XX 28-FEB-2001; 2001US-0079649P.
 XX 01-MAR-2001; 2001WO-US006520.
 XX 09-MAR-2001; 2001US-0080270P.
 XX 14-MAR-2001; 2001US-00808689.
 XX 22-MAR-2001; 2001US-00816744.
 XX 05-APR-2001; 2001US-0082836P.
 XX 10-MAY-2001; 2001US-0085428P.
 XX 25-MAY-2001; 2001US-00866034.
 XX 25-MAY-2001; 2001WO-US017092.
 XX 30-MAY-2001; 2001US-00870574.
 XX 01-JUN-2001; 2001WO-US017443.
 XX 20-JUN-2001; 2001WO-US017890.
 XX (GERTH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERRA) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURNE) GURNEY A L.

PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANU) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 PI Baker KP, Ferrara N, Gerber H, Gertitsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 DR WPI; 2002-171999/22.
 DR P-PSDB; ABB95545.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 1, Fig 245; 567pp; English.
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 SQ
 Alignment Scores:
 Pred. No.: 2.55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-063-734-122 (1-243) x ABL95683 (1-1257)
 QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 138 ATGGGACCCAGGAGCCCGCGCTCCCGACGCGCTCCGCGCTCTGCTCTG 197
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLyGlyLeuGlnLeuAla 40
 Db 198 CTGCTGAGCTGCTCCCGCGCTCGAGCCGCTCTGAGATCCCAAGGGGAAACCAAGGCG 257
 QY 41 GlnLeuArgGlnArgGluValValAspLeuTYRANGLYMETCYLeuGlnGlyProAla 60
 Db 258 CAGCTCCGGAGAGGAGAGTGTGTGACCTGTAATAGAAATGTCTTCAAGGGGCGACGA 317
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTYRProGlyIle 80
 Db 318 GGAGTCCCTGTGTGAGACCGGAGCCCTCGGGGCAATGTATTCCGGGTACACCTGGGATC 377
 QY 81 ProGlyArgAspGlyPheLeuGlyGluValGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 378 CCAAGTCGGGATGATTCACAAAGAGAAAGAGGAGAAATCTGAGAGGAAACCTTGAAGAG 437
 QY 101 SerTyrPheProAsnTYRLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 Db 438 TCCTGACACCCCACTACAGAGAGTTCATGAGATTCATTGATTTATGCAATAGATCTT 497
 QY 121 GlyValIleAlaGluCysTyrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 498 GGAATAATTCGGAAGTGTACATTTCACAAAGATGCTCAATATGCTCAAGAGTTTG 557
 QY 141 PheSerGlySerLeuArgLeuLeuCYeArgAsnAlaCysCysGlnArgTyrPheThr 160

Db 558 TTCAGTGGCTCACTTGGCTTAAATGAGAAATGCATGCTGCGGTTGATTTCACA 617
Qy 161 PheASnglYAlaGluCyseSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCAATGAGACTTAATGTTGAGACCTTCCCAATGAACTTAATTAATTGGACCAA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgTherSerValGluGlyLeu 200
Db 678 GGAAGCCTGAATGATTCACACATTAAATTCATGCACTTCTGTGGAGAGACTT 737
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGATTCGTGCTGATGAGATGATGATGATGATGATGATGATGATGATGAT 797
Qy 221 TyrProIleGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAGAGATGCTTCTACTGATGAGATGATGATGATGATGATGATGATGATGAA 857
Qy 241 LeuProIys 243
Db 858 CTACCAAAA 866
RESULT 24
ACa89557
ID ACa89557 standard; cDNA; 1257 BP.
XX ACA89557;
AC 10-JUL-2003 (first entry)
XX
DT
XX
XX
DE cDNA encoding human PRO polypeptide #183.
XX
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytoskeletal; antiarthritic; osteopathic; gene therapy; gene;
KW 88.
XX
OS Homo sapiens.
XX
PN US2003036141-A1.
XX
XX
PD 20-FEB-2003.
XX
PF 01-JUL-2002; 2002US-00187597.
XX
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 17-DEC-1997; 97US-0069425P.
PR 18-DEC-1997; 97US-0069870P.
PR 10-MAR-1998; 97US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 31-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 01-APR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 08-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081039P.
PR 09-APR-1998; 98US-0081070P.
PR 15-APR-1998; 98US-0081195P.
PR 21-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 22-APR-1998; 98US-0082699P.
PR 22-APR-1998; 98US-0082704P.
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PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087088P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 05-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.

XX 01-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) CDNA #183.
DE Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX Homo sapiens.
XX US2003036146-A1.
PD 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187603.
XX 26-JUN-1998; 98US-00105413.
XX 16-SEP-1998; 98WO-US019330.
XX 07-OCT-1998; 98US-00168978.
XX 07-OCT-1998; 98WO-US021141.
XX 06-NOV-1998; 98US-00187368.
XX 01-DEC-1998; 98WO-US025108.
XX 07-DEC-1998; 98US-00202054.
XX 03-MAR-1999; 99US-00254311.
XX 08-MAR-1999; 99WO-US005028.
XX 14-MAY-1999; 99US-00311832.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012552.
XX 25-AUG-1999; 99US-00380137.
XX 25-AUG-1999; 99US-00380138.
XX 25-AUG-1999; 99US-00380139.
XX 25-AUG-1999; 99WO-US080142.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 18-OCT-1999; 99US-00403297.
XX 12-NOV-1999; 99US-00423844.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028551.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US00341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US01941.
XX 02-JUN-2000; 2000WO-US015264.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000WO-US023328.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 22-MAR-2001; 2001US-00816744.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 01-JUN-2001; 2001WO-US017800.
XX 05-JUN-2001; 2001US-00874503.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.

PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX (GENTH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI, 2003-332034/31.
DR P-PSDB; AB086375.
XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting
PT the presence of tumor in a mammal.
XX Claim 2; Fig 365; 707pp; English.
XX The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1567 or
CC PRO4333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumor in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating the
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a CDNA encoding a PRO
CC protein
XX
XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
Pred. No.: 2 55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-063-734-122 (1-243) x ACN73567 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCGACCCGAGGGCCCGCCGCTCCCGACGCGGCTCCGCGGCTCTGCTGCTCG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProLysGlyIlyleGlnLysAla 40
DB 198 CTGCTGACAGCTGCGCGCGCTCGACGCGCTCTGAGATCCCAAGGGGAGGAAAGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaPheLysIlyAsnGlyMetCysLeuGlnIlyProAla 60
DB 258 CAGCTCCGCGACAGGAGGTGGTGGACCTGTATATGAAATGATGCTTCAAGGGCCACCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTGCTGCTGCTGCGACGCGAGCGCCCTGGGCCAAATGATATCCCGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLysGlyGlnLysGlyGlnCysLeuArgGlnSerPheGlnGlu 100
DB 378 CCAGGTCCGGATGATGATCAAGAGAGAAAGGGGGAATCTCGAGGAAAGCTTTGAGGAG 437
QY 101 SerTPThrProAsnIlyLysGlnCysSerTPSerSerLeuAsnIlyGlyIlyAspLeu 120
DB 438 TCCTGACACCCCACTACAGCAGGTTCATGAGTTCATGAAATTAATGCAATGATCTT 497
QY 121 GlyIlyIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATATGCGGAGTGTACATTTACAAGATGCGTTCAATATGCTCTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 558 TTCAGTGGCTCTGCTGCTGCTAAATGCAAGAAATCAAGCTGTGAGCTGTGATTTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIlyLysAspGln 180
DB 618 TTCATGAGACTGATGATTCAGACCTCTCCCTTACAGCTTAAATTAATTTTGGACCA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGluLys 200
DB 678 GGAAGCCCTGAAATGAATTCACAAATTAATTAATTCATGACACTCTCTGGAAGGACTT 737
QY 201 CysGlnGlyIlyleGlyAlaGlyLeuValAspValAlaIleIlyValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATTTGCTGTGATTTAGTGAGTGTGATCTGAGGTGGACTGTTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleGlnGlu 240
DB 798 TACCCCAAGAGATCTCTACTGATGATGAATTCAGTTTCTGCACTATTAAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 26
ACA05882
ID ACA05882 standard; cDNA, 1257 BP.
XX
AC ACA05882;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #183.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO, TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
FN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PT

PR 07-OCT-1998; 98US-00166978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99US-00380142.
PR 15-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001WO-US021066.
PR 30-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Goddard PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332039/31.
XX P-PDB; AB067588.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT

PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
PS Claim 2, Fig 365; 706pp; English.

XX The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide; a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide; a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide; a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX

SO Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 2,55e-104 | Length: | 1257 |
|------------------------|-----------|---------------|------|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ACA05882 (1-1257)

```
QY 1 MetATGProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGGCCCCCGCCCTCCCGACGGCTCCGCGCCCTCCGCTCCG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProArgGlyLeuGln 40
DB 198 CTCTCTCAGCTGCCCCCGCCCTCGAGCGCTTGAAGTCCCAAGGGGAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValValaAspLeuTyAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGGAGGGAGGGGTGGTGGACCTGTATATGAAATGTCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValLeuProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGGTGGAGACGGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlnSerPheGlnGln 100
DB 378 CCAAGTCCGGATGATTCAAAGAGAAAGAGGGAATGTTGAGGAAACCTTTGAGGAG 437
QY 101 SerTyrThrProAlaTyrIleGlnCysSerTyrSerSerLeuAlaTyrGlyIleAspLeu 120
DB 438 TCTTGACACCCCACTACAAAGAGTGTTCATGAGTTCAATTAATGATATGCAATATCTT 497
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATATGGAGAGTATCATTACAAAGATCGTTCAATATGTCCTCAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 558 TTGAGTGGCTCACTTGGCTAAATGCAAAATGATGCTGTCAGCGCTTGATTTTCA 617
QY 161 PheAsnGlyValaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleIleIle 180
DB 618 TTCAATGAGAGCTGAATGTTACAGAGCTCTTCCCATTTGAAGCTAATTAATTTTGA 677
```

```
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 678 GAAAGCCCTGAATGATTCACAACTATTAATTCATCGACATCTTCTGTGAGAGACTT 737
QY 201 CysGlnGlyIleGlyValaGlyLeuValaAlaIleTyrValGlyThrCysSerAsp 220
DB 738 TTGGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCGGTTGGCACTGTTCA 797
QY 221 TyrProGlyValaAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGln 240
DB 798 TACCCAAAAGAGAGTCTTCTACTGGATGAAATTCAGTTTCTCGCATTAATTAAGA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 27
ACA6716
ID ACA6716 standard; cDNA; 1257 BP.
XX
AC ACA6716;
XX
DT 23-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO protein #183.
XX
KW Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
XX liver; PRO; gene therapy; gene; ss.
XX
PN Homo sapiens.
XX
PD US2003036137-A1.
XX
20-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184640.
XX
26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 30-DEC-1999; 99WO-US028551.
PR 03-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 02-JUN-2000; 2000MO-US015264.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001MO-US019592.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941932.
 PR 29-AUG-2001; 2001MO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-342038/32.
 DR P-PSDB; ABU0616.

XX
 PT Three hundred and five nucleic acids encoding secreted and transmembrane
 PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 PT cervical or liver tumors.
 XX
 PS Claim 2; Fig 365; 708bp; English.
 XX

XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions
 CC of the present invention are useful for the diagnosis, prevention and/or
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,
 CC rectal, cervical or liver tumors. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The present
 CC sequence represents a cDNA encoding a human PRO polypeptide of the
 CC invention
 XX

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-063-734-122 (1-243) x ACA66716 (1-1257)

QY 1 MethArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 138 ATGGAGCCCGAGGCGCGCGCTCCCGAGCGGCTCCGCGGCTCTGCTCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyLeuGlyAla 40
 Db 198 CTCTCTCACTGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCGC 257
 QY 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 Db 258 CAGCTCCGAGGAGGAGGAGGTGTGAGCTGATATATGATATGCTTCAAGAGGCCAGCA 317
 QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 318 GAGATGCTGTGTGAGAGCGGAGCGCTGGGGCCCAATGTTATTCGGGGTACACTGGGATC 377
 QY 81 ProGlyValArgAspGlyPheLeuGlyGlyIleGlyGlyCysLeuArgGlyGlySerPheGlyGly 100
 Db 378 CCAGTCCGAGATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
 QY 101 SerTyrThrProLeuTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 Db 438 TCTTGAGACCCCACTACACAGCTGTTCATGAGATTGATTAATGAGCATGATCTT 497
 QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 498 GGGAAATTTGCGAGTGTACATTTACAAAGATGGCTTCAATAGTCTCTAAGAGTTTG 557
 QY 141 PheSerGlySerLeuArgLeuLeuCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 Db 558 TTCAGTGGCTCACTTCGGCTTAAATGAGAAATGCAATGCAATGCTGAGCTGTGATTTCA 617
 QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleTyrLeuAspGln 180
 Db 618 TTCAATGAGCTGATATTTGAGAGCTCTTCCATGGAAGCTATTAATTTATTTGAGACCA 677
 QY 181 GlySerProGlnLeuAsnSerThrIleAsnIleArgThrSerSerValGlyLeu 200
 Db 678 GGAAGCCCTGAAATGATTCACATTAATTAATTCATGCACTTCTCTGTGAGAGACTT 737
 QY 201 CysGlyGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
 Db 738 TGTAAAGAAATTTGATGTGATTAATGATGATGATGATGATGATGATGATGATGAT 797
 QY 221 TyrProGlyAlaAspAlaSerThrGlyTyrPheSerValSerArgIleIleGlnGlu 240
 Db 798 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAA 857
 QY 241 LeuProLeu 243
 Db 858 CTACCAAAA 866
 RESULT 28
 ID ACA91224 standard; cDNA; 1257 BP.
 XX ACA91224;
 AC AC91224;
 DT 11-JUL-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1550 cDNA.
 KW Human; secreted and transmembrane protein; PRO; antibody therapy;
 KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
 XX Homo sapiens.
 XX US2003018173-A1.
 XX 23-JAN-2003.
 XX
 XX 01-MAY-2002; 2002US-00063515.
 XX 06-DEC-2001; 2001US-00006867.
 XX
 PA (GETH) GENENTECH INC.

XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
XX WPI: 2003-401702/38.
DR P-PSDB; AB090936.

PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.

PS Disclosure: Fig 121; 345bp; English.

XX The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostic, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x ACA91224 (1-1257)

QY 1 MetAAGProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCCG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlnGlyLeuGlnVala 40
DB 198 CTGCTGCACTGCGCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGAGAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValaValaLeuLeuYrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 GAGCTCCGCGAGGGAGGTGGTGGACCTGTATGATGATGCTTACAGGGCCAGCA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGAGTCCCTGCTGAGACGGAGCCCTGGGGCCAAATGATTCCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlnCysLeuArgGlnSerPheGlnGln 100
DB 378 CCAAGTCGGGATGATTCAGAGGAAAGGGGAAATGCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTrpLysGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120
DB 438 TCCTGGAGACCCCACTACAGACAGAGTGTTCATGAGTTCATTGATTAATGCAATGATCTT 497
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAAGAAATGCGAGAGTACATTACAAAGATCGCTTCAAAATGATGCTTAAAGATTG 557
QY 141 PheSerGlySerLeuArgLeuLeuValCysArgAsnAlaCysCysGlnArgTrpTrpPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTAAATATCAGAAATGACAGTGTGAGGTTGGATTTTCA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTrpLeuAspGln 180
DB 618 TTCAATGAGAGCTGAATGTTCAAGGACCTTCCATTGAGGCTATATTATTGAGCA 677

QY 161 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 678 GGAAGCCCTGGAATATTAATTCACATTATTCACACTTCTTCTGTGAGAGGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValaAspValaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGAAATTGGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGln 240
DB 798 TACCCAAAGAGAGTCTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866
RESULT 29
ACDB1601
ID ACDB1601 standard; cDNA; 1257 BP.
XX ACDB1601;
AC ACDB1601;
XX 18-SEP-2003 (first entry)
DT 18-SEP-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1550.
XX
KW Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KW cytosolic.
XX
OS Homo sapiens.
XX US2003009013-A1.
PN
XX
PD 09-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063519.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
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PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000MO-US004341.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
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PR 22-MAY-2000; 2000MO-US014042.
PR 02-JUN-2000; 2000MO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 18-SEP-2000; 2000US-0064610.
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PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001WO-US004520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854288.
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PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.

PR 18-JUN-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GERTH) GENENTECH INC.
XX

PI Easton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-447384/42.
DR P-PSDB; ABO33995.XX

PT New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.

PS Disclosure; Fig 121; 223pp; English.

XX The invention relates to an antibody that binds to a secreted or
XX transmembrane protein designated PRO1446 appearing as ABO33941. The
XX protein is one of 84 PRO polypeptides which (along with their encoding
XX nucleic acids) are disclosed in the specification. The methods and
XX compositions of the present invention are useful for the preparation of a
XX medicament for the treatment of disorders associated with the aberrant
XX expression or activity of the PRO polypeptide, such as tumor conditions
XX and cancer. They can also be used to generate transgenic or knockout
XX animals useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides and encoding nucleic acids can be used as
XX molecular weight markers for protein electrophoresis, chromosome
XX identification and tissue typing. The antibodies may be used in various
XX diagnostic, competitive binding and/or immunoprecipitation assays. The
XX present sequence encodes a PRO polypeptide

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-063-734-122 (1-243) x ACD81601 (1-1257)

QY 1 MetATGProGInGlyProAlaIaSerProGInATGLeuATGlyLeuLeuLeuLeu 20
DB 138 ATGCAATCCCAAGGCGCCGCGCTCCCGCAGCGCGCTCCGCGCTCCGCTCG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProLyAGlyLeuGInuAla 40
DB 198 CTGCTGCACTGCGCCGCGCGCTCCGCGCTCCGCGCTCCGCGCTCCGCTCG 257
QY 41 GInLeuATGInATGAGlyValAlaIaSerLeuTyraAnglyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGAGTGTGAGCTGTATATGAAATGCTTCAAGGGCGAGCA 317
QY 61 G1yValProG1yATGAspG1ySerProG1yAlaIaSerValIleProG1yTyrPheG1yLe 80
DB 318 GAGAGGCTGTGTCAGAGAGGAGCCCTGCGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProG1yATGAspG1yPheLeuG1yGluIyG1yCysLeuATGAspG1ySerPheG1yGlu 100
DB 378 CCAGGTGGGAGTGAATTCMAAGAGAAAGGGGAAATGTCGAGGAGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrlYsGInCysSerTrpSerSerLeuAsnTyrlYsG1yIlaSpLeu 120
DB 438 TCCCGACACCACTACAGCACTGTTTCATGAGGTTCAATGAAATTTATGCAATGATCTT 497
QY 121 G1yLyAlleAlaG1yCysTrpPheThrLySerArGserAsnSerAlaLeuATGValLeu 140
DB 498 GGGAAATTCGAGGTACTTATTAACAAGATGGCTTCAAAATGCTCTTAAGATTITG 557

QY 141 PheSerGlySerLeuATGLeuIyCysArGAsnAlaCysCysGInATGTrpTyrlPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAGAAATGAGTGTGCGCTTGATTTTACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln 180
DB 618 TTCATGAGAGCTGAATGATTCAGAGACTTCTCCATTAAGCTTAATTTATTTGGACCA 677
QY 181 G1ySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluIyLeu 200
DB 678 GGAAGCCCTGAATGAATTAACAATTAATTAATGCACTTCTTGCGAAGACATT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGAAATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLyG1yAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAGAGAGATGCTTCTTACGATGAGATTCGATTCGATTCGATTCGATTCG 857
QY 241 LeuProLyS 243
DB 858 CTACCCAAA 866
RESULT 30
ID ACF20291
ACF20291 standard; cDNA; 1257 BP.
ACF20291;
18-SEP-2003 (first entry)
DE XX
XX Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnery; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003040063-A1.
XX
XX 27-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183006.
XX
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059263P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
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XX 28-OCT-1997; 97US-0063540P.
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XX 11-DEC-1997; 97US-0068335P.
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XX 10-MAR-1998; 98US-0077450P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091010P.
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PR 02-JUL-1998; 98US-0091632P.
PR 04-AUG-1998; 98US-0094006P.
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PR 18-AUG-1998; 98US-0096949P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.

PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
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PR 01-OCT-1998; 98US-0102687P.

Alignment Scores:

| Pred. No.: | 2,55e-104 | Length: | 1257 |
|------------------------|-----------|---------------|------|
| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ACF20291 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCAGGCGCCCGCCTCCCGCAGCGCTCCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVal 40
DB 198 CTGCTGAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGGCGC 257
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGTGTGAGCTGTATATGATGATGCTTACAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValLeuProGlyTyrProGlyTyr 80
DB 318 GAGTGTCTGTGTGAGAGCGGAGCCCTGGGGCCCAATGTATTCGGGTTCACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyCysLeuArgGlnSerPheGlnGly 100
DB 378 CCAGGTGCGGATGATTCAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTyrTyrGlnCysSerTrpSerSerLeuAsnTyrGlyTyrLeuAspLeu 120
DB 438 TCTTGAGACCCCACTACAGACAGTGTTCATGAGATTCATTGATATGAGCATATGATCTT 497
QY 121 GlyTyrGlnAlaGlnCysThrPheThrTyrMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATATGCGGAGGTGATTCATTACAAAGATCGCTTCAAAATGATGCTTAAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
DB 558 TTCAGTGTCACTTCGCTAAATGACAGAAATGATGCTGTCAAGCTTGATTTTCA 617
QY 161 PheAsnGlyValAlaGlyCysSerGlyProLeuProGlnGlnAlaLeuLeuLeuLeu 180
DB 618 TTCATGAGAGCTGATGATTCAGAGACCTCTTCCCATTTGAAGCTATATATTTTGAACCA 677
QY 181 GlySerProGlnMetAsnSerThrTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200
DB 678 GGAACCCCTGAATGATTCACCAATTAATTCATTCGACCTCTTCTGTGAGAGACTT 737
QY 201 CysGlnGlyTyrGlyValGlyLeuValAspValAlaLeuTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAGAAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrTyrTyrAsnSerValSerArgTyrLeuLeuGlnGlu 240
DB 798 TACCAAAAGAGAGATGCTTCTTACATGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProGly 243
DB 858 CTACCAAA 866

RESULT 31
ACF19677
ID ACF19677 standard; cDNA; 1257 BP.

XX AC ACF19677;
XX 17-SEP-2003 (first entry)
DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antitubercular; vulnerability; gene therapy; gene; ss.
XX Homo sapiens.
XX
OS
PN US2003040064-A1.
XX
PD 27-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183008.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
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PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069455P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
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PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
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PR 17-SEP-1998; 98US-0100683P.
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Alignment Scores:

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| Pred. No.: | 2 55e-104 | Length: | 1257 |
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| Percent Similarity: | 100.00% | Conservative: | 0 |
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US-10-063-734-122 (1-243) x ACP19677 (1-1257)

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| QY | 1 | MetArgProGInGlyProAlaIaSerProGInArgLeuArgGlyLeuLeuLeuLeu | 20 |
| DB | 138 | ATGCGACCCCAAGGCGCGCGCTCCCGGACGCGGCTCCGCGGCTCCTGCTGCTCG | 197 |
| QY | 21 | LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProGlyGlyLeuGInLeu | 40 |
| DB | 198 | CTGCTGCACCTCCCGCGCGCTCGACGCGCTTGAGATCCCGACAGGGAAGCAAGCGG | 257 |
| QY | 41 | GInLeuArgGInArgGlyValValaIaSpLeuTyzAaGInGlyMetCysLeuGInGlyProAla | 60 |

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| PR | 28-OCT-1997 | 9.75US-00635644 |
| PR | 28-OCT-1997 | 9.75US-00635644 |
| PR | 29-OCT-1997 | 9.75US-00637504 |
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| PR | 31-OCT-1997 | 9.75US-00641033 |
| PR | 13-NOV-1997 | 9.75US-00651131 |
| PR | 24-NOV-1997 | 9.75US-00664656 |
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| PR | 11-DEC-1997 | 9.75US-00667722 |
| PR | 12-DEC-1997 | 9.75US-00693555 |
| PR | 18-DEC-1997 | 9.75US-00694255 |
| PR | 10-MAR-1998 | 9.75US-00698070 |
| PR | 11-MAR-1998 | 9.75US-00774500 |
| PR | 11-MAR-1998 | 9.75US-00776322 |
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| PR | 01-APR-1998 | 9.75US-00801944 |
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PR 22-JUN-1998; 98US-0090246P.
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Alignment Scores:

Pred. No.: 2,55e-104
Score: 1301.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 8
Matches: 1257
Conservative: 243
Mismatches: 0
Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x ACD21965 (1-1257)

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlnGlnysAla 40
DB 198 CTGCTGACAGCTCCCGCGCGCGCTGAGCGCTGAGATCCCAAGGAGAAAGGCGG 257
QY 41 GlnLeuArgGlnArgGlnValValAspleuTyraGlnGlyMetCysLeuGlnGlnProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGAGCTGTGACCTGTATTAATGAGATGCTTACAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
DB 318 GAGAGTCCCTGTGAGACGCGAGCCCTGCGGCAATGATATCCCGGATACACCTGGAGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlnGlyGlnGlyGlnGlnGlnGlnGlnGlnGlnGln 100
DB 378 CCAAGTCGGGAGATTCACAGAGAAAGGAGGAGATGCTGAGGAAAGCTTGAAGAG 437
QY 101 SerTyrThrProAsnTyrIysGlnCysSerTyrPserSerLeuAsnTyrGlyIleAspleu 120
DB 438 TCCTGGACACCACTACACAGAGATGATGAGATTCATTAATTAATGACATATTCAT 497
QY 121 GlyValIleAlaGlnCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTCGAGAGTACATTACAAAGATGCGTCAAAATGATGCTTAAGAGATTGG 557
QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 558 TTCAGTGGCTCACTTCGCTAAATGCAAGATGATGCTGACGCTTGATTTGACA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATGAGCTGAATGTTGAGAGACCTTCCCATTTGAAGCTATTAATTTGACCA 677

QY 181 GlycerProGluMeAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAACCCCTGGAATGATTCACCATTAATTCATCGACTCTTCTGTGAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAlaIleTPValGlyThCysSerAsp 220
Db 738 TGTGAAGAAATGGTGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleGluGly 240
Db 798 TACCAAAAGAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 33
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ID ACFI3130 standard; cDNA; 1257 BP.
XX
ACFI3130;
XX
DT 13-SEP-2003 (first entry)
XX
DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antirheumatic; vulnery; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036160-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188781.
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PR 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0062250P.
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Alignment Scores:
Pred. No.: 2,556-104 Length: 1257
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 LeuLeuGlnLeuProhlaaIaSerSerIaSerGlnLeuLeuLeu 40
DB 198 CTGCTGACAGCTGCGCGCGCTGAGCGCTGAGATCCCAAGGAGAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValaIaSerLeuLeuLeuLeuLeuLeu 60
DB 258 CAGCTCCCGCAGAGGAGGTGTGACCTGTATATGAGATGCTTACAGGCGCAGA 317
QY 61 GlyValProglnglyArgAspGlySerProglnglyAlaSerValIleProglngly 80
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QY 81 ProglnglyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGly 100
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QY 101 SerTPThProAsnTyrIleGlnCysSerTPSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCTTGACACCCCACTACACAGCAGCTGTATGAGATTCATTAAATTAAGCATATCTT 497
QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerSerAlaLeuArgValLeu 140
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QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 558 TTCAGTGCCTGCTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
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QY 241 LeuProGly 243
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DT 30-AUG-2003 (first entry)
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XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;

KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KM prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

PN US2003044925-A1.

XX 06-MAR-2003.

PF 25-JUN-2002; 2002US-00180560.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

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QY 61 GlnValProGlnArgAspGlySerProGlnAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGGTGAAGACCGGACCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
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QY 141 PheSerGlySerLeuArgLeuValCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCATGCTGCACGCTTGATTTTACACA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 618 TTCAATGAGCTGAATGTTCAGGACCTCTCCCATTTGAAGCTATTAATTTTGAACCA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
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DB 738 TGTGAAGAAATGGTGTCTGATTAATGATGATGTTGCTATCTGGCTTGACATTTGCAGAT 797
QY 221 TyrProGlyValAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGln 240
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XX 19-SEP-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antithrptic; vulnerary; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX US2003054474-A1.
XX 20-MAR-2003.
XX
XX 22-JUL-2002; 2002US-00201530.
XX
XX 22-JUN-1998; 98US-0090254P.
XX 02-JUN-1999; 99WO-US012252.
XX 25-AUG-1999; 99US-00380137.
XX 28-FEB-2001; 2001WO-US006520.
XX 15-JAN-2002; 2002US-00052586.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-503631/47.
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PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.

PS Disclosure; Fig 121; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 2,55e-104 | Length: | 1257 |
| Score: | 1301.00 | Matches: | 243 |
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| Query Match: | 100.00% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ACA60423 (1-1257)

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DB      138 ATGCCAGCCACGAGGCCCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyAla 40
DB      198 CTGCTGACACTGCGCCGCGCTGAGCGGCTCTGAGATCCCAAGGAGGAAAGGCGG 257
QY      41 GlnLeuArgGlnArgGlnValValAlaPleuYrAsnGlyMetCysLeuGlnGlyProAla 60
DB      258 CAGCTCCGCGCAGAGGAGGTGGTGGACCTGTATATGAGATGTCTTCAAGGCCAGCA 317
QY      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB      318 GGAGTCCCTGCTGAGACGGGAGCCCTGGGGCCATGTTATTCGGGTACACTGGGATC 377
QY      81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB      378 CCAAGTCGGAGTGGATTCAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 437
QY      101 SerTyrThrProAsnTyrIlysgInCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB      438 TCCTGACACCCCACTACACAGCAGCTTCAAGATGATTCATGATTAATGATGATTC 497
QY      121 GlyValIleAlaGlnCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
DB      498 GGGAAATATGGGAGTGTACATTATTAAGATGCGTTCAAAATGTGCTCTTAAGATTGG 557
QY      141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB      558 TTCAGTGGCTCACTTGGCTAAATGACAGAAATGATGCTGAGGCTGGATATTTCA 617
QY      161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleIleIle 180
DB      618 TTCAGAGGAGCTGAATGCTTCAAGACCTCTTCCATTGAAGCTATTAATTTTGGACCA 677
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIle 200
DB      678 GGAAGCCCTGAATGAATTCACAAATTAATTCATGCACTTCTTCTGAGAAAGACTT 737
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QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
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QY      221 TyrProGlyValAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
DB      798 TACCCAAAAGAGAGTCTTCACTGATGGAATTCAGTTTCGCATCATTAATTGAAGA 857
QY      241 LeuProGly 243
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ID ACA72339 standard; cDNA; 1257 BP.
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DT 30-JUN-2003 (first entry)
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KW chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knock-out animal; tumour; gene; ss.
XX Homo sapiens.
XX US2003032114-A1.
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PD 13-FEB-2003.
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PF 20-JUN-2002; 2002US-00176919.
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 8
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x ACD04863 (1-1257)

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGly 40
DB 198 CTGCTCAGCTGCGCCGCGCTGAGCGCTCTGAGATGCCCAAGGGAAGCAAGGCGG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGTGTGAGCTGTATATGAGATGTCTTACAGGGCCAGCA 317
QY 61 GlyValProGlyYArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
DB 318 GAGATCTCTGCTGACACCGGACCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyYArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CAGGTCGGGATGATTTCAAGAGGAAAGGGGAAATGCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTyrThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
DB 438 TCTGTGACACCCCACTACAGAGCTGTATCATGAGTTCAATGATATGATGATGATCTT 497
QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTTGCGGAGTGTACATTACAAAGATCGTTCAATGCTCTCAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
DB 558 TTCAGTGGCTCACTTGGCTAAATGCAAGAAATGATGCTGAGGCTTGGATTTTCA 617
QY 161 PheAsnGlyValAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 618 TTCAAAGGAGCTGAATGTTCAAGACCTCTCCATGAGCTATTAATTTATTTGAGCAA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200
DB 678 GGAAGCCCTGAAATGAAATTCACAAATTAATTCATGACATCTCTCTGAGAGACTT 737
QY 201 CysGlnGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCTGGCTTGGCACTTCTCAGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGlnGln 240
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QY 241 LeuProIle 243
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DT 06-AUG-2003 (first entry)
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DE Human; ss; gene therapy; tumour necrosis factor alpha; TNF-alpha;
XX Chondrocyte stimulation; tumour; tissue typing; gene.
XX Homo sapiens.
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XX US2003032101-A1.
PN 13-FEB-2003.
XX 17-JUN-2002; 2002US-00173695.
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Alignment Scores:

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Pred. No.: 2.55e-104
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Query Match: 100.00%
DB: 8
Gaps: 0

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US-10-063-734-122 (1-243) x ACD04863 (1-1257)

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QY 61 GlyValProGlyArgAspGlySerProGlyAlaSerValIleProGlyThrProGlyIle 80
Db 318 GGAAGTCCCTGCTGCGAGCGGAGCCCTTGAGGSCAATGTATTCGGGTACACCTGGGATC 377
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Alignment Scores:

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| Score: | 1301.00 | Matches: | 243 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
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US-10-063-734-122 (1-243) x ACD18324 (1-1257)

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DB 438 TCCGAGACCCACACACACAG 497
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DB 498 GGGAAATTCGAG 557
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DB 558 TTCAGTGGCTCACTTCGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
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RESULT 40
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09-AUG-2003 (first entry)

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Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.
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XX US2003040054-A1.
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PD 27-FEB-2003.
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Score: 1301.00 Matches: 243
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x ACD08331 (1-1257)

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DT 09-JUL-2003 (first entry)
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KW Human; se; gene therapy; chondrocyte stimulation; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour detection;
KW tissue typing; gene.
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OS Homo sapiens.
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PN US2003036133-A1.
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XX 20-FEB-2003.
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XX 27-JUN-2002; 2002US-00184630.
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| PR | 01-OCT-1998 | 98US-0102684P |
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| PR | 07-OCT-1998 | 98US-0106197P |

Alignment Scores:

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| Pred. No.: | 2.55e-104 | length: | 125 |
| Score: | 1301.00 | Matches: | 243 |
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| Best Local Similarity: | 100.00% | Mismatches: | 0 |
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| DB: | 8 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ACA88765 (1-1257)

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| QY | MetArgProGlnIleProIleaaIaSerProGlnIleGluArgIleuLeuLeuLeuLeu | 20 |
| Db | 138 ATGCGACCCAGGAGCCCGCGCTTCCCGCAGCGGCTCCGGGCTCTCTGCTCTG | 197 |
| QY | 21 LeuLeuGlnLeuProIleProSerSerIleSerGluIleProGlyIleGlnIleGln | 40 |
| Db | 198 CTGCTGAGCTGCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGACCAAGCG | 257 |
| QY | 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnIleProIle | 60 |
| Db | 258 CAGCTCCGACAGGGAGGTGGTGACCTGTATATGAAATGTGCTTCAAGGGCCAGCA | 317 |
| QY | 61 GlyValProGlyIleArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle | 80 |
| Db | 318 GGAATCTCTGGTCGAGACCGGAGCCCTGGGGCAATGTATTCCGGGACACCTGGGATC | 377 |
| QY | 81 ProGlyIleArgAspGlyIlePheIleGlyGlnIleGlyCysLeuArgGlySerPheGlnGlu | 100 |
| Db | 378 CCAAGTCGGGATGGATTCAAAGAGAAAGGGGGAATCTGAGAGGAAGCTTTGAGGAG | 437 |
| QY | 101 SerThrThrProAsnThrIleGlnCysSerThrSerSerLeuAsnTyrGlyIleAspLeu | 120 |
| Db | 438 TCTTGACACCCCACTACAGACGAGTTCATGAGATTCATTGAATTTGCGATGAGATCTT | 497 |
| QY | 121 GlyIleValIleArgIleCysThrPheThrIleMetArgSerAsnSerIleAlaMetValLeu | 140 |
| Db | 498 GCGAAATATGGGAGTGATCATTTTCAAGATGCGTTCAATATAGTGGCTTCAAGAGTTTGG | 557 |

QY 141 PHeSerGIySeLeuAArgLeuLyCyArGAsAlaLyCySeGInArGTpTyPHeThr 160
Db 558 TTCATGGCTCACTTCGGCTTAATTCAGAAATGCATGCTGCACCGTTGGATTTTACA 617
QY 161 PHeAnGIyAlaGluCySeSerGIyProLeuProIleGluAlaIleIleTyLeuAspGln 180
Db 618 TTCATATGAGGTGATGATGTTCAAGACCTTCCTCCATGTAAGCATATATATTTTGGACCA 677
QY 181 GIySeProGIumeLaseSerThrIleAnIleHArgThSeSeValGluGlu 200
Db 678 GGAAGCCCTGAATGAATTCACAAATTAATTCATCCGACTCTTCGTGGAAAGACAT 737
QY 201 CySeGluGIyIleGIyAlaGluLeuValAspValAlaIleTPValGIyThrCySeSerAsp 220
Db 738 TGTCGAAGAAATGGTGTGATTAAGGATGTTGCATCTGGGCTTGGCATCTTTCAGAT 797
QY 221 TyProLySeGIyaSpAlaSeThrNGlyTPaSeSerValSeArgIleIleIleGluGlu 240
Db 798 TACCAAAAGAGATGCTTCTACTGATGGATTCAGTTCTCCGACATATTATTGAAGA 857
QY 241 LeuProLyS 243
Db 858 CTACCAAAA 866

RESULT 42

ACA70207
ID ACA70207 standard; cDNA; 1257 BP.
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RESULT 43
ACD12429
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PR 01-OCT-1998; 98US-0102684P.
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Alignment Scores:

| Score: | 2.55e-104 | length: | 1257 |
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| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-10-063-734-122 (1-243) x ACD12429 (1-1257)

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInIleProIlyGlyyGInySAIa 40
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QY 41 GInLeuAArgGInAArgIuValIaIaSerLeuTyraAngIyMetCysLeuGInGlyProAla 60

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Qy 61 G1yAlProglYArAspGlySerProglYAlaAsnValIlePeproglYThrProglYIle 80
Db 318 GGAAGTGGCTGGTGCAGACGGAGGCCCTGGGCCCAATGTATTTCGGGGTACACCTGGGATC 377
Qy 81 ProglYArAspGlyPheIlyGlyIlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
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Qy 241 LeuProIys 243
Db 858 CTACCAAAA 866

RESULT 44
ACCT74344
ID ACC74344 standard; cDNA; 1257 BP.
XX ACCT4344;
AC ACCT4344;
XX 28-JUN-2003 (first entry)
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DE
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnerary; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX US2003027275-A1.
PN
XX 06-FEB-2003.
PD
XX 20-JUN-2002; 2002US-00176918.
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PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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KW gene mapping; transgenic animal; knockout animal; tissue typing;
KW chromosome identification; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW gene therapy; gene; ss.
OS Homo sapiens.
XX
PN US2003036118-A1.
XX
PD 20-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176760.
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PR 15-JAN-2002; 2002US-00052586.
XX
XX
PA (GENTH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z,
XX
DR MPI; 2003-402071/38.
XX
XX P-PSDB; ABO19293.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, chromosome identification, tissue typing, for detecting
PT the presence of tumor in a mammal, or as hybridization probes in gene
PT mapping.
PS Claim 2; SEQ ID NO 365; 707bp; English.
XX
XX The invention describes a novel isolated PRO polypeptide. The PRO
CC polypeptide or anti-PRO antibody is useful for preparing a medicament for
CC treating a condition that is responsive to the PRO polypeptide or anti-
CC PRO antibody. The PRO nucleotide sequences are useful as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful for detecting
CC the presence of tumour in a mammal, stimulating proliferation or
CC differentiation of chondrocyte cells, stimulating the release of tumour
CC necrosis factor-alpha from human blood, in gene therapy, or as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
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Alignment Scores:
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 Score: 1301.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 8
 Gaps: 0

US-10-063-734-122 (1-243) x ACD18017 (1-1257)

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 QY 21 LeuLeuGlnLeuProAlaPProSerSerAlaSerGluLeuProGlyGlyLeuAla 40
 DB 198 CTGCTGCAAGCTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 258 CAGCTCCGCGAGAGGAGGAGTGGTGGACCTGTATATGATGATGATCCCAAGGGAAGCAAGGCG 317
 QY 61 GlyValProGlnArgAspGlySerProGlyAlaAsnValIleProGlyTyrProGlyIle 80
 DB 318 GGAATGCTGTGTGAACCGGAGCCCTCGGCGCAATGTATTCCGGTACACTGGAGATC 377
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 378 CCAAGTCGGATGATGATTCACAAAGGAAAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAG 437
 QY 101 SerTyrThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 438 TCCTGGACACCCCAACTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
 QY 121 GlyLeuIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 498 GGGAAATTCGGAGATGATTCATTACAAAGATGCTTCAATAGTCTTCAAGGATTTTG 557
 QY 141 PheSerGlySerLeuArgLeuLeuCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAGATGATGATGATGATGATGATGATGATGATGAT 617
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
 DB 618 TTCATGAGCTGAATGTTCAGACCTTCCCTTCAACTATTAATTATTGAGCAAA 677
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgHisSerValGluGlyLeu 200
 DB 678 GGAAGCCCTGAAATTAATTCACAAATTAATTCATGATGATGATGATGATGATGATGATGAT 737
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAsp 220
 DB 738 TGTGAAGGAATGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
 QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGlu 240
 DB 798 TACCAAAAGAGATGCTTCTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 857

OY 241 Leuprolide 243
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 ID ACC88304 standard; cDNA; 1257 BP.
 AC ACC88304;
 XX
 XX 05-AUG-2003 (first entry)
 DT
 DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
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 XX Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antitumor; veterinary; gene therapy; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003036148-A1.
 PN
 PD 20-FEB-2003.
 XX
 XX 02-JUL-2002; 2002US-00187743.
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Alignment Scores:

Pred. No.: 2,55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-063-734-122 (1-243) x ACC88304 (1-1257)

QY 1 MetArgProGInGlyProAlaIaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20

DB 138 ATGCACCCACGAGCCCGCCGCTCCCGAGGCGGCTCCGCTGCTCTG 197
 QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProGlyGlyGInLeuAla 40
 DB 198 CTGCTGCAGCTGCCGCCGCCGCTCGAGCGCTCTAGATCCCAAGGGAAGCAAGCG 257
 QY 41 GInLeuArgGInArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGInGlyProAla 60
 DB 258 CAGCTCCGACAGGAGGAGGTGTGACCTGTATATGAAATGTCTTACAGGCGCAGCA 317
 QY 61 GlyValProGlyArgArgGlySerProGlyValAlaSerValIleProGlyThrProGlyIle 80
 DB 318 GGAATGCTGTGTCCAGACGAGAGCGCCCTGGGCCCATATGTATTCGGGTACACCTGGGATC 377
 QY 81 ProGlyArgArgGlyPheLeuGlyGlyGluGlyCysLeuArgGlySerPheGluGlu 100
 DB 378 CCAGGTCCGGATGATTCATAAGAGAAAGGGGGAATGTGAGGGAACCTTGAGAG 437
 QY 101 SerThrProAsnTyrIleGlnCysSerThrSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 438 TCTGGACACCACTACAGACAGTGTTCATGAGTTCATTGAAATATGACATAGATCTT 497
 QY 121 GlyIysIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 498 GGGAATAATTCGGAGTGTACATTTACAAAGATCGCTTCAATATGTCTTAAAGATTGG 557
 QY 141 PheSerGlySerLeuAlaGluCysArgAsnAlaCysGlyGlnArgTrpThrPheThr 160
 DB 558 TTCAGTGTCTCATTCCGCTTAAATGACAAATGATGTCAGCGCTTGATTTACA 617
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
 DB 618 TTCATGAGAGTGAATTTACAGACCTCTTCCATTGAAGCTTAAATTAATTTGACCAA 677
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
 DB 678 GGAAGCCCTGAATGATTCACAAATTAATTCATGCGACCTTCTGTGAGAGACTT 737
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
 DB 738 TGTGAGGAATGTGTGTGATTAAGATGTTGATGTGATGTGGCATCTGTTCACAT 797
 QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGlu 240
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 QY 241 LeuProIys 243
 DB 858 CTACCAAAA 866

RESULT 49

ACD21658 ID ACD21658 standard; cDNA, 1257 BP.

ACD21658; XX

27-AUG-2003 (first entry) XX

Human secreted/transmembrane protein (PRO) cDNA #183. DE

Human, Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
 prostate tumour; rectal tumour; cervical tumour; liver tumour. KW

Homo sapiens. OS

US2003040060-A1. PN

27-FEB-2003. PD

24-JUN-2002; 2002US-00179525. PF

XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
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Alignment Scores:

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US-10-063-734-122 (1-243) x ACD21658 (1-1257)

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 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuGlnLeu 40
 DB 198 CTGCTGCAAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGGAAAGGCG 257
 QY 41 GlnLeuArgGlnArgGlyValAlaAspLeuTyraGlyMetCysLeuGlnGlyProAla 60
 DB 258 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGGAATGCTTCAAGGCGCAGCA 317
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 DB 318 GAGAGCGCTGTGTGAGACGAGGAGCCCTGCGGCAATGTATTCGCGTACACTGGGATC 377
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyLeuGlyGlyCysLeuArgGlySerPheGlnGly 100
 DB 378 CCAGGTCCGGATGATTCAGAGAGAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAG 437
 QY 101 SerThrProArgThrIleGlyGlnCysSerTrpSerSerLeuAsnTyraGlyIleAspLeu 120
 DB 438 TCTGGACACCACTACACAGACAGTGTTCATGATGATTAATGATGATGATGATGAT 497
 QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 498 GGGAAATTCGGAGGTGTACATTTCAGAAAGATGCGTCAATATGCTTAAGAGTTTG 557

QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
 DB 558 TTCAGTGGCTCACTTCGGTAAATGAGAAATGATCTCTGACGCTTGATTTGACA 617
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyraAspGln 180
 DB 618 TTCATGAGAGTGTGAATGTTCCAGAGACCTCTCCATTAAGCTATTAATTTGACCAA 677
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
 DB 678 GGAAGCCCTGGAATGAATTCACATTAATTAATTCACCTCTCTGTTGGAAGACTT 737
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
 DB 738 TGTGAAGAAATTTGGTGTGATTAAGTGTGATGATGATGATGATGATGATGATGAT 797
 QY 221 TyrProLysGlyAspAlaSerThrGlyThrAsnSerValSerArgIleIleGluGlu 240
 DB 798 TACCAAAAGAGATCTTCTACTGATGAGAAATTCAGTTCTGCAATTAATTAAGAA 857
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 AC 28-AUG-2003 (first entry)
 DT 28-AUG-2003 (first entry)
 DE Human secreted/transmembrane protein (PRO) cDNA #183.
 XX Human, gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
 OS Homo sapiens.
 XX US2003044916-A1.
 FN 06-MAR-2003.
 PD 20-JUN-2002; 2002US-00176484.
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Alignment Scores:

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US-10-063-734-122 (1-243) x ACD18725 (1-1257)

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| QY | 21 | LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLysGlyLysGlnLysAla | 40 |
| DB | 198 | CTGCTGAGCTGCCCGCGCTGAGGCTCTGAGATCCCAAGGGGAGCAAAAGCG | 257 |
| QY | 41 | GlnLeuArgGlnArgGlyValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla | 60 |
| DB | 258 | CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGCCAGCA | 317 |
| QY | 61 | GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle | 80 |
| DB | 318 | GAGTCTCCTGTGTGAGACGGAGCCCTGGGGCCCAATGTATTCGGGTACACCTGGGATC | 377 |
| QY | 81 | ProGlyArgAspGlyPheLysGlyGlyLysGlyLysCysLeuArgGlnSerPheGlnGln | 100 |
| DB | 378 | CCAGTCGGGATGATTCAAAGAGAGAAAGGGGATGTCTAGGAGAAAGCTTTGAGAG | 437 |
| QY | 101 | SerTyrThrProAsnTyrLysGlnCysSerTyrPheSerSerLeuAsnTyrGlyIleAspLeu | 120 |
| DB | 438 | TCTTGACACCCCAACATCAAGAGGTGTGATGATGATTCATTAATGATGATGATCTT | 497 |
| QY | 121 | GlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu | 140 |
| DB | 498 | GGGAAATTCGCGAGGTGATTCATTAACAAAGATGCTTCAATAGTCTTAAAGATTG | 557 |
| QY | 141 | PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr | 160 |
| DB | 558 | TTCAGTGGCTCACTTCGGCTAAATGACAAATGATGCTGTCAAGTTGTGATTTTCA | 617 |
| QY | 161 | PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln | 180 |
| DB | 618 | TTCAATGAGACTGAAATGTCAAGACCTTCCCATTTGAAGCTATTAATTTATTTGACCA | 677 |
| QY | 181 | GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu | 200 |
| DB | 678 | GGAAGCCCTGAATGAATTCACCAATTAATATTCACCTTCTTGTGAGAGACTT | 737 |
| QY | 201 | CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp | 220 |
| DB | 738 | TGTGAGGAATGTGTGTGATTAATGATGTGTGATCTGATCTGGGTGACATTTGATGAT | 797 |
| QY | 221 | TyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu | 240 |
| DB | 798 | TACCAAAAGAGATGCTTCTACTGATGATGATGATTCAGTTCTCGCATCATTAATGAAGA | 857 |
| QY | 241 | LeuProLys 243 | |
| DB | 858 | CTACCAAAA 866 | |

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 25, 2004, 05:33:57 ; Search time 3198 Seconds
(without alignments)
2768.873 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MRPOGPASPRRLRGILL.....GDASTGMSVSRRIIEELPK 243

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Database :

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3: gb_est3: *
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7: gb_est7: *
8: gb_gse1: *
9: gb_gse2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1294 | 99.5 | 1103 | 3 | CR594803 full-length |
| 3 | 1294 | 99.5 | 1189 | 3 | CR596030 full-length |
| 4 | 1294 | 99.5 | 1207 | 3 | CR605392 full-length |
| 5 | 1289 | 99.1 | 1111 | 3 | CR612318 full-length |
| 6 | 1284 | 98.7 | 1288 | 3 | BC021025 Homo sapi |
| 7 | 1272 | 97.8 | 732 | 9 | AY399085 Pan trogl |
| 8 | 1267 | 97.4 | 827 | 1 | AL544722 |
| 9 | 1266 | 97.3 | 1100 | 1 | AL551834 |

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| 11 | 1254 | 96.4 | 1098 | 1 | AL532456 |
| 12 | 1248 | 95.9 | 986 | 5 | BX387691 |
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| 14 | 1207 | 92.8 | 849 | 6 | CB201936 |
| 15 | 1205 | 92.6 | 738 | 9 | AY399086 |
| 16 | 1201 | 92.3 | 1161 | 3 | AK003674 |
| 17 | 1195 | 91.9 | 716 | 6 | CA413294 |
| 18 | 1181 | 90.8 | 1168 | 3 | AK076498 |
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| 49 | 905 | 69.1 | 688 | 2 | BE176395 |
| 50 | 899 | 69.1 | 1087 | 1 | BU111109 |
| 51 | 899 | 69.1 | 878 | 6 | CB589580 |
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| 53 | 893.5 | 68.7 | 1023 | 4 | BG421228 |
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| 56 | 868 | 66.7 | 508 | 5 | BX517433 |
| 57 | 865 | 66.3 | 534 | 5 | BU700520 |
| 58 | 850 | 65.3 | 508 | 5 | CK689987 |
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| 60 | 842.5 | 64.8 | 676 | 5 | BU133087 |
| 61 | 839 | 64.5 | 937 | 5 | CF180990 |
| 62 | 833 | 64.0 | 590 | 6 | BB614200 |
| 63 | 824 | 63.3 | 666 | 2 | BB614200 |
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| 66 | 782.5 | 60.1 | 1073 | 5 | BU510203 |
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| 68 | 775.5 | 59.6 | 644 | 7 | CF359545 |
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| BM560093 | AGENCOURT |
| AL532456 | AGENCOURT |
| BX387691 | BX387691 |
| CR592899 | full-length |
| CB201936 | AGENCOURT |
| AY399086 | Mus muscu |
| AK003674 | Mus muscu |
| CA413294 | UI-H-EZO- |
| AK076498 | Mus muscu |
| AL553798 | AL553798 |
| BX386416 | BX386416 |
| BI108785 | 602895273 |
| BX386415 | BX386415 |
| BU624465 | UI-H-FGI- |
| AL553771 | AL553771 |
| BQ425098 | AGENCOURT |
| BU624261 | UI-H-FGI- |
| BM915926 | AGENCOURT |
| BQ425266 | AGENCOURT |
| AL575307 | AL575307 |
| AL564395 | AL564395 |
| BM915288 | AGENCOURT |
| BQ574527 | UI-H-EZ1- |
| BQ648112 | AGENCOURT |
| AL585129 | AL585129 |
| BU27614 | 603003696 |
| CN394776 | 170004245 |
| BU408973 | 603159022 |
| BU278868 | 603602753 |
| CB959810 | AGENCOURT |
| BX265931 | BX265931 |
| BU128948 | 603114409 |
| BU141753 | 603136852 |
| BE896915 | 601439457 |
| BU275159 | 603414514 |
| BX884616 | BX884616 |
| CN394775 | 170005325 |
| BX299779 | AGENCOURT |
| BQ424201 | AGENCOURT |
| BE176395 | 603047656 |
| BE87335 | 601276538 |
| BU111109 | 603111109 |
| CB589580 | AGENCOURT |
| CB991371 | AGENCOURT |
| BG421228 | 602451719 |
| CK698549 | ZF101-P00 |
| CN394773 | 170006001 |
| BX517433 | BX517433 |
| BU700520 | UI-M-DJ1- |
| CK689987 | ZF101-P00 |
| BU326094 | 603491057 |
| BU133087 | 603120752 |
| CF180990 | 817779 MA |
| BB614200 | BB614200 |
| BB614200 | DG11-93m2 |
| BE691507 | 602247681 |
| BX387690 | BX387690 |
| BU510203 | BU510203 |
| CO681284 | DG11-127n |
| CF359545 | 820803 MA |
| CB056888 | NISC 1432 |
| BU409295 | 603157529 |
| BU270206 | 603509637 |
| CR408276 | CR408276 |
| CO696320 | DG11-96D2 |
| BU408671 | 603157531 |
| AT963298 | wt61b12. x |
| BU472792 | 603365437 |
| AL570753 | AL570753 |
| BU470778 | 603760468 |
| BU504730 | 60304730 |
| BM701829 | UI-E-COI- |
| BU469630 | 603762249 |

| | | | | | | | | |
|---|-----|-------|------|------|---|----------|--------|-----------|
| C | 83 | 723 | 55.6 | 611 | 7 | CF360739 | 822264 | MA |
| | 84 | 716.5 | 55.1 | 1113 | 4 | BM463039 | | AGENCOURT |
| | 85 | 704 | 54.1 | 407 | 1 | AV649395 | | AV649395 |
| | 86 | 703 | 54.0 | 518 | 6 | CB998290 | | AGENCOURT |
| | 87 | 680 | 52.3 | 386 | 1 | AD695311 | | AGENCOURT |
| | 88 | 676 | 52.0 | 963 | 7 | CF376690 | | AGENCOURT |
| | 89 | 674 | 51.8 | 513 | 7 | CF359477 | | AGENCOURT |
| | 90 | 674 | 51.8 | 655 | 7 | CO794642 | | AGENCOURT |
| | 91 | 670.5 | 51.5 | 1265 | 6 | CB197831 | | AGENCOURT |
| | 92 | 667 | 51.3 | 583 | 4 | BJ490431 | | AGENCOURT |
| | 93 | 662 | 50.9 | 542 | 4 | CD741549 | | AGENCOURT |
| | 94 | 643 | 49.9 | 744 | 6 | CD741549 | | AGENCOURT |
| | 95 | 643 | 49.4 | 399 | 5 | BM924504 | | AGENCOURT |
| | 96 | 640 | 49.2 | 387 | 1 | AA335862 | | AGENCOURT |
| | 97 | 640 | 49.2 | 464 | 2 | BE169370 | | AGENCOURT |
| | 98 | 639 | 48.9 | 366 | 6 | CO1758 | | AGENCOURT |
| | 99 | 636 | 48.1 | 1159 | 5 | BM55899 | | AGENCOURT |
| | 100 | 631.5 | 48.5 | 378 | 1 | AD697355 | | AGENCOURT |

ALIGNMENTS

RESULT 1
AY399084
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY399084
Homo sapiens CTRC1 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
AY399084
GI:39755073
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 732)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.D.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene titers

JOURNAL
PUBMED

Science 302 (5652), 1960-1963 (2003)
14671302

REFERENCE
AUTHORS

2 (bases 1 to 732)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.D.,
Adams, M.D. and Cargill, M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers

FEATURES
source

1..732
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/gene="CTRCL1"
/locus_tag="HCM0106"

gene

ORIGIN

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 2,12e-113 | Length: | 732 |
| Score: | 1294.00 | Matches: | 242 |
| Best Local Similarity: | 99.59% | Conservative: | 0 |
| Best Local Similarity: | 99.59% | Mismatches: | 1 |
| Query Match: | 99.46% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-10-063-734-122 (1-243) x AY399084 (1-732)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetArgProGInGlyProAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu | 20 |
| Db | 1 | ATGCGACCCCAAGGCGCCCGCCCTCCCGAGGCGGCTCCGCGGCTCTGCTGCTCTG | 60 |
| Qy | 21 | LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla | 40 |
| Db | 61 | CTGCTGAGCTGCTGCGCGCGCTGAGCGCTCTGAGATGCCCAAGGGAAGCAAGGCG | 120 |
| Qy | 41 | GInLeuArgGInArgGluValAlaSerLeuTyranGlyMetCysLeuGInGlyProAla | 60 |
| Db | 121 | CAGCTCCGCGAGAGGAGAGTGGTGGACCTGTAATGAAATGCTTACAGGCGCCAGCA | 180 |
| Qy | 61 | GlyValProGInArgAspGlySerProGlyAlaSerValIleProGlyThrProGlyIle | 80 |
| Db | 181 | GGAGTGCCTGCTGAGACGGAGCGCTGGGCGCAATGATTCGGGATACCTGGGATC | 240 |
| Qy | 81 | ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly | 100 |
| Db | 241 | CCAGCTCCGAGATGATTCATCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG | 300 |
| Qy | 101 | SerThrProAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly | 120 |
| Db | 301 | TCTGAGACACCACTCAAGCAAGTGTTCATGAGTTCATGATTAATGATGATGATTC | 360 |
| Qy | 121 | GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu | 140 |
| Db | 361 | GGGAAATTCGCGAGTGTACATTTACAAAGATCGTTCAATAGCTCTTAAGAGTTTG | 420 |
| Qy | 141 | PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlyGlnArgTrpPheThr | 160 |
| Db | 421 | TTCAGTGGCTCACTTCGGCTAAATGAGAAATGATGATGATGATGATGATGATGAT | 480 |
| Qy | 161 | PheAsnGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleLeuLeuAspGln | 180 |
| Db | 481 | TTCATGAGCTGAATGTATGAGACCTCTCCATGAGATTAATTAATTAATTAATTAAT | 540 |
| Qy | 181 | GlySerProGInLeuSerThrIleAsnIleArgThrSerSerValGluGlyLeu | 200 |
| Db | 541 | GGAGCCCTGAATGATTCACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT | 600 |
| Qy | 201 | CysGluGlyIleGlyAlaGlyLeuValAlaIleIleIleIleIleIleIleIleIleIle | 220 |
| Db | 601 | TGTGAAGATGTGTCTGATTAAGATGATGATGATGATGATGATGATGATGATGAT | 660 |
| Qy | 221 | TyrProGlyIleAspLeuSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu | 240 |
| Db | 661 | TACCAAAAGAGATGCTTCTACTGATGAATTCAGTTTCGCATCATTAATTAATTAAT | 720 |
| Qy | 241 | LeuProIle 243 | |
| Db | 721 | CTACCAAAA 729 | |

RESULT 2

LOCUS

DEFINITION
Full-length cDNA clone CS01022YF04 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

Contact : Feng Liang Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1103)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
Source Location/Qualifiers

1..1103
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI022YF04"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 3,69e-113 Length: 1103
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 3 Gaps: 0

US-10-063-734-122 (1-243) x CR594803 (1-1103)

OY 1 MetatgProglng1yProalalaserProglng1yLeuleuleu 20
DB 70 ATGCCAAGCCAGAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 129
OY 21 LeuleuGlnLeuProalProseSerAlaserGulieProlysglyyGlnyala 40
DB 130 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCGAGATCCCAAGGGAAGCAAGGCG 189
OY 41 GlnleuArgGlnArgGlnValValAspleuTyraAnglyMerCyLeuGlnGlyProala 60
DB 190 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAGATGTCTTACAGGGCCAGCA 249
OY 61 G1yValProgl1yArgAsp1ySerProgl1yAlaenVal1leProgl1yThrProgl1y 80
DB 250 GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGCAATCCGGTACACCTGGAGATC 309
OY 81 Progl1yArgAsp1yPheLyseGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 310 CCAGGTGGGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
OY 101 SerTPThProAsnTy 120
DB 370 TCCTGAGACCCCAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
OY 121 G1yLy1leAlaGlyCyThrPheThlyMerArgSerAsnSerAlaLeuArgVal1leu 140
DB 430 GGGAAATTTGCGGAGGTACATTTACAAAGATCGTCAATATGTCCTTAAGAGTTTGG 489
OY 141 PheSerGlySerLeuArgLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 160
DB 490 TTCAGTGAGCTCACTTGGCTAAATATGCAAAATGATGCTGTCAGCGTTGATTTCA 549
OY 161 PheAsnGlyAlaGlyCySerGlyProleuPro1leGlnAla1le1leTyTyTyTyTy 180
DB 550 TTCAAATGGAGTGAATGTTCAAGACCTCTTCCATTTGAAGCTATATTTATTTGACCA 609
OY 181 G1ySerProgl1yMerAsnSerThr1leAsn1le1leArgThrSerSerValG1yGlyLeu 200
DB 610 GGAAGCCCTGAATGAATTCACAAATTAATTATTCACGACCTTCTTCTGGAAGACATT 669
OY 201 CyG1yGlyTy1leGlyAlaGlyLeuValAspValAla1leTyTyTyTyTyTyTyTyTy 220
DB 670 TCGAAGAAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729

OY 221 TyrProLyGlyAspAlaSerThrGlyTyraSerValSerArg1le1leGlyGln 240
DB 730 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 789

OY 241 LeuProLy 243
DB 790 CTACCAAAA 798

RESULT 3

CR596030 1189 bp mRNA linear HTC 21-JUL-2004

LOCUS full-length cDNA clone CSODI061YA20 of Placenta Cot 25-normalized

DEFINITION of Homo sapiens (human).

ACCESSION CR596030.1 GI:50476837

VERSION CR596030.1 GI:50476837

KEYWORDS HTC; CDS; cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1189)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue

2 (bases 1 to 1189)
Genoscope.

REFERENCE 2 (bases 1 to 1189)
Genoscope.

AUTHORS Direct Submission

TITLE Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
Source Location/Qualifiers

1..1189
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI061YA20"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Alignment Scores:
Pred. No.: 4,09e-113 Length: 1189
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 3 Gaps: 0

US-10-063-734-122 (1-243) x CR596030 (1-1189)

OY 1 MetatgProglng1yProalalaserProglng1yLeuleuleu 20
DB 94 ATGCCAAGCCAGAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 153
OY 21 LeuleuGlnLeuProalProseSerAlaserGulieProlysglyyGlnyala 40
DB 154 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCGAGATCCCAAGGGAAGCAAGGCG 213
OY 41 GlnleuArgGlnArgGlnValValAspleuTyraAnglyMerCyLeuGlnGlyProala 60
DB 214 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAAATGCTTTCACAGGGCCAGCA 273
OY 61 G1yValProgl1yArgAsp1ySerProgl1yAlaenVal1leProgl1yThrProgl1y 80
DB 274 GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGAGATTCGGGTACACCTGGATC 333

| | | | | |
|------------|--|---|--|------|
| Oy | | 81 | ProglYAAGAggAglyPhelyAgglYgltulysgtYgtlucysleuaArgIuseRpheluglu | 100% |
| Dd | | 334 | CcAGGTCCGATGATGATTCAAAAGGAAGAAAAAGGGGGGAAATCTCGAAGGAAACGTTTGAGAG | 39% |
| Oy | | 101 | SerTPnHrProAsnTYrFlyeGlncYseRTripSerSerleuaenTYrGLyllleaSleu | 120% |
| Dd | | 394 | TCTCGAACACCACCTACAGCAGTTCACAGAGTTCATGAGATTAATGCGATRGACTT | 453% |
| Oy | | 121 | GLYlsIIeaIagIucYvethrPheThrlYswelArgerSaenseralaleuaArgValIeu | 140% |
| Dd | | 454 | GCGAAATTCGGAGATGGATGATCAATTTACAAAAGATGGCTCAATAGTGCCTTAAGATTG | 513% |
| Oy | | 141 | PheSerGIyseRIeuaArgleuLYeCyArGaSmAlaCYeCySGlna-gLrPYrPheThr | 160% |
| Dd | | 514 | TTCAGTGGCTCACTTCGGCTMAATGAGAATGACAATGCAATGCTGACGCTTGATTCACA | 573% |
| Oy | | 161 | PheasnGLYlaGluCYeSerGIYProleuProIllegualalIetIryleuaSpGln | 180% |
| Dd | | 574 | TTCAATGAGCTGATGATGATTCAGACGCCCTTCCTCCATTAACCTMAATTTATTTGACCAA | 633% |
| Oy | | 181 | GIYserProGIuMetAenSerThrlIeaSnll ehiSarGrhSerSeVaIGlugIueu | 200% |
| Dd | | 634 | GGAAGCCCTGAATGAATTCACACTTAATTCATCATGCACTTCTTGIGGAAGACATT | 693% |
| Oy | | 201 | CYeGlnGIylIlegIvalagIyleuValaspaValalIetTpValglYthrCYseRaap | 220% |
| Dd | | 694 | TGTGAAGAAATGGTGTGATTAAGTGAGATGTGCTATCGCGTGTGACTTGTCAGAT | 753% |
| Oy | | 221 | TYrProLySIyaSpAlaseRThrgLYrTPASerSeVaIserrglIelleIlegluIn | 240% |
| Dd | | 754 | TACCCAAGAGATGTTCTTACTGATGAGAAATTCACTTTCGCATCATTAATGAGA | 813% |
| Oy | | 241 | IeuPrOlys 243 | |
| Dd | | 814 | CTACCAAAA 822 | |
| RESULT 4 | | | | |
| LOCUS | | CR605392 | | |
| DEFINITION | | full-length cDNA clone CS0D1037YD19 of Placenta Cot 25-normalized | | |
| ACCESSION | | CR605392 | | |
| VERSION | | CR605392.1 | | |
| KEYWORDS | | HTC; CNSLT - cDNA. | | |
| SOURCE | | Homo sapiens (human) | | |
| ORGANISM | | Homo sapiens | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | |
| AUTHORS | | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| JOURNAL | | Li,W.B., Gruber,C., Jessee,J. and Polayes,D. | | |
| REMARK | | Full-length cDNA libraries and normalization | | |
| | | Unpublished | | |
| | | Contact : Feng Liang Email : fliang@lifetech.com URL : | | |
| | | http://fulllength.invitrogen.com/Invitrogen Corporation 1600 | | |
| | | Paraday Avenue | | |
| | | 2 (bases 1 to 1207) | | |
| | | Genoscope. | | |
| REFERENCE | | Direct Submission | | |
| AUTHORS | | Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : | | |
| TITLE | | BP 191 J1006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr | | |
| JOURNAL | | - Web : www.genoscope.cns.fr) | | |
| | | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime | | |
| | | into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library | | |
| | | was normalized. Library was constructed by Life Technologies, a | | |
| | | division of Invitrogen. | | |
| FEATURES | | location/Qualifiers | | |
| SOURCE | | 1..1207 | | |
| | | /organism="Homo sapiens" | | |
| | | /mol_type="mRNA" | | |
| | | /db_xref="taxon:9606" | | |
| | | /clone="CS0D1037YD19" | | |

| ORIGIN | /tissue type="Placenta Cot 25-normalized" | /plasmid="pCMVSPORT_6" |
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| Alignment Scores: | 4.17e-113 | 1207 |
| Pred. No.: | 1294.00 | Matches: 242 |
| Score: | 99.59% | Conservative: 0 |
| Percent Similarity: | 99.59% | Mismatches: 1 |
| Best Local Similarity: | 99.59% | Indels: 0 |
| Query Match: | 99.46% | Gaps: 0 |
| DB: | 3 | |
| US-10-063-734-122 (1-243) x CR605392 (1-1207) | | |
| QY | 1 MetArpProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeuLeu 20 | |
| Db | 94 ATGCGACCCAGGAGCCGCCGCCCTCCCGGAGGGGCTCCGAGGCTCTGCTCTCG 15 | |
| QY | 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGlyAla 40 | |
| Db | 154 CTGCTGCACTCCGCCGCCCTCGAGGCGCTCTGATCTCCCAAGGGAGGAAAGCG 21 | |
| QY | 41 GlnLeuArgGlnArgGlyValValAspLeuThrAspGlyMetCysLeuGlnGlyProAla 60 | |
| Db | 214 CAGCTCCGCGAAGGAGAGTGTGTGACCTGTATTAAGAAATGCTTCAAGAGGCGACCA 27 | |
| QY | 61 GlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80 | |
| Db | 274 GGAAGTCCCTGTCGAGACGGGAGCCCTGGGGCCCAATGGCATTCGCGGTACCTGGATC 33 | |
| QY | 81 ProGlyValArgAspGlyPheLeuGlyGlyLeuGlyGlyCysLeuArgGlySerPheGlnGlu 100 | |
| Db | 334 CCAGGTCCGGAGTTCATTAAGAGAAAGGGGAAATGTCTAAGGAAAGCTTTGAGAG 39 | |
| QY | 101 SerTPThrProAsnThrValGlyGlnCysSerTyrSerSerLeuAsnThrGlyIleAspLeu 120 | |
| Db | 394 TCCTTGAAACCCCACTCAAGACAGTGTTCATGAGAGTTCAATTATGCGATGATCTT 45 | |
| QY | 121 GlyValIleAlaGluCysThrPheMetIleMetArgSerSerAsnSerAlaLeuValLeu 140 | |
| Db | 454 GGGAAATTTGGCGAGTGTACATTTTCAAGAAAGCGTTCAAATAGGCTCTAAGAGTTTG 51 | |
| QY | 141 PheSerGlySerLeuArgLeuLeuCysValArgAsnAlaCysCysGlnArgTyrPheThr 160 | |
| Db | 514 TTCAGTGGCTCACCTTCGGCTAAATCAAGAAATGCGTGTGACAGCTGTGATTTACA 57 | |
| QY | 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180 | |
| Db | 574 TTCATGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTAATAATTTATTGGACCA 63 | |
| QY | 181 GlySerProGluLeuSerAsnThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200 | |
| Db | 634 GGAAGCCCTGAATGAATCAACAATATATATTATTCATGCACTTTCTGCGAAGACCTT 69 | |
| QY | 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220 | |
| Db | 694 TGTAAAGAAATTTGCTGTGATTAAGATGTGTCTAATCTGGGTGGTACCTTTGTACAGAT 75 | |
| QY | 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGlu 240 | |
| Db | 754 TACCCAAAGAGATGCTCTCACTGAGATGGAATTCAGTTTCTCGCATCATTAATTGAAGA 81 | |
| QY | 241 LeuProGlyS 243 | |
| Db | 814 CTACCAAAA 822 | |
| RESULT 5 | | |
| CR612318 | 1111 bp | MRNA |
| LOCUS | full-length cDNA clone | linear |
| DEFINITION | CSDBM041N20 of Fetal liver of Homo sapiens | |
| ACCESSION | CR612318 | |
| VERSION | 1 | |

| KEYWORDS | HTC: CNSLT. cDNA. |
|---|--|
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| AUTHORS | Li, W.B., Gruber, C., Jesssee, J. and Polayes, D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished |
| REMARK | Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue |
| REFERENCE | 2 (bases 1 to 1111) |
| AUTHORS | Genoscope. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : secref@genoscope.cns.fr) |
| COMMENT | Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five primers end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. |
| FEATURES | Location/Qualifiers |
| source | 1..1111 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODM014YN20" /issue_type="Petal 1 liver" /plasmid="pCMVSPORT_6" |
| ORIGIN | |
| Alignment Scores: | |
| Pred. No.: | 1,12e-112 Length: 1111 |
| Score: | 1289.00 Matches: 241 |
| Percent Similarity: | 99.59% Conservative: 0 |
| Best Local Similarity: | 99.59% Mismatches: 1 |
| Query Match: | 99.08% Indels: 0 |
| DB: | 3 Gaps: 0 |
| US-10-063-734-122 (1-243) x CR612318 (1-1111) | |
| QY | 2 ArgProGInGlyProAlaIaSerProGInArgLeuArgGlyLeuLeuLeuLeuLeu 21 |
| DB | 2 CGACCCGAGGGCCCGCGCCCTCCCGGAGCGGCTCCGCGGCTCTGCTGCTGCTG 61 |
| QY | 22 LeuGInLeuProAlaProSerSerAlaSerGulIleProGlyIleGlyAlaGln 41 |
| DB | 62 CTGCGAGTCCCGCCGCGCTCGAGCCCTCTGAGATCCCGAGGGGAGAACAAAGCGCAG 121 |
| QY | 42 LeuArgGInArgGInValValAspLeuIyrAenGlyMetCysLeuGInGlyProAlaGly 61 |
| DB | 122 CTCGCGCAGAGGAGAGCTGTGAGCTGTATATGAAATGTGCTTACAAAGGCCACAGGA 181 |
| QY | 62 ValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIlePro 81 |
| DB | 182 GTGCCTGTGTCGAGAGCGGAGCCCTGTGGGCCAATGGCAATTCCGGGTACACCTGGAGTCCA 241 |
| QY | 82 GlyArgAspGlyPheLeuGlyGlyIleGlyGlyIleGlyCysLeuArgGlyIleSerPheGluGlnSer 101 |
| DB | 242 GGTCCGGATGCAATTCMAAGGAGAAAGGGGAGATCTCGAGCGGAAGCTTTGACGAGTCC 301 |
| QY | 102 TrpThrProAsnIyrLeuGlnCysSerIrpSerSerLeuAsnIyrGlyIleAspLeuGly 121 |
| DB | 302 TGGACACCCAACTACAGCAGTGTTCATGGAATTCATTGAATTATGCAATGATCTTGGG 361 |
| QY | 122 LysIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeuPhe 141 |
| DB | 362 AAAATTGGGAGTGTACATTTTACAAAGATGCGTTCAAAATAGTGTCTAAAGAGTTTGTTC 421 |
| QY | 142 SerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysGlyGlnArgTrpIyrPheThrPhe 161 |

| | | | | |
|------------|---|----------------------|---|------------------------|
| Db | | 422 | AGTGGCTCACCATTGGCGCTAAATGAGAANAATGCANCTGTGACGGTGTAATTCACATTC | 481 |
| Oy | | 162 | AamglYalagluCySsergIylProleuprolleglualallelelyrleuaesrgIngly | 181 |
| Db | | 482 | AATGAGACTGAATGTTTACGACCTCTCCATGGAACCTAATATTATTTGGACAAGCA | 541 |
| Oy | | 182 | SerProglUmeVenseRtrrlleAmllleHlsargrThsSerSerValglUglUeCys | 201 |
| Db | | 542 | AGCCCTGAATGAATTCACACATTAATTCATGCCACTTCTCTGTGGANGAACCTTGT | 601 |
| Oy | | 202 | GluGlYllleglYalaglYleuValaspValalaletrPvalglYTrCySserAspTy | 221 |
| Db | | 602 | GAAGCATTTGGTGTGGATTAGTGGATGCTTGCTATCTGGGTGGTACTTGTTCAGATTAC | 661 |
| Oy | | 222 | ProLyglYalpalaSerThrglYTPasnservalSerargllellelgluGluleu | 241 |
| Db | | 662 | CCAATAAGAGATGCTTCTTACTGATGAGATTCAGTTCTCGCATCATTAATTTGAAGAATA | 721 |
| Oy | | 242 | Prolys 243 | |
| Db | | 722 | CCAAAA 727 | |
| RESULT 6 | | | | |
| LOCUS | BC021025 | 1288 bp | mRNA | linear HTC 04-AUG-2004 |
| DEFINITION | Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA clone IMAGE:3617432). | | | |
| ACCESSION | BC021025 | | | |
| VERSION | BC021025.1 | GI:18045042 | | |
| KEYWORDS | HTC. | | | |
| SOURCE | Homo sapiens (human) | | | |
| ORGANISM | Homo sapiens | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| AUTHORS | Strausberg,R.L., Reingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Bueltow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Steplaton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toehiyuki,S., Cannicini,P., Prange,C., Kaha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wexler,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimmood,J., Schmutz,J., Myers,R.M., Buttefield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marrs,M.A. | | | |
| TITLE | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences | | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. | 99 (26), 16899-16903 | (2002) | |
| PUBMED | 12477932 | | | |
| REFERENCE | 2 (bases 1 to 1288) | | | |
| AUTHORS | Director MGC Project. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, | | | |
| REMARK | USA | | | |
| COMMENT | NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: ATCC/DCTP/DMP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbio.org | | | |

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLML at: <http://image.lhml.gov>
Series: IRAL Plate: 24 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923988
This clone has the following problem: no cloning site / microdeletion.

FEATURES
Source
Location/Qualifiers

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/organism="Homo sapiens"
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/clone="IMAGE:3617432"
/issue_type="Skin, melanotic melanoma."
/clone_id="NH MGC_20"
/lab_host="DH10B-R"
/note="Vector: pOT87"

ORIGIN

Alignment Scores:
Pred. No.: 4,12e-112 Length: 1288
Score: 1284.00 Matches: 241
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 98.69% Indels: 0
Gaps: 3

US-10-063-734-122 (1-243) x BC021025 (1-1288)

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGln 40
Db 203 CTGCTGCACTGCGCCCGCCCTGCAAGCGCTCTGCAATCCCAAGGGAAGCAAAAGCG 262
QY 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTYRAsnGlyMetCysLeuGlnGlyProAla 60
Db 263 CAGCTCCCGCAAGGAGGAGGTGGGACCTGTATTAATGAATGGCTTCAAGGCGCAGCA 322
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 323 GGAAGTCCCTGCTCGAAGACGGAGCCCTGGGSCCAATGGCATTCCGGTACACCTGGAGTC 382
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlnGlyCysLeuArgGlySerPheGlnGln 100
Db 383 CCAGGTCCGGATGATTCAAGAGAAAGGGGAGATGCTGAGGAAAGCTTTGAGGAG 442
QY 101 SerTPHrProAsnTYRLeuGlnCysSerTPSerserLeuAsnTYRLeuAspLeu 120
Db 443 TCTTGGACACCCCACTACAGAGAGTTCATGAGATTCATGAATTAATGATAGATCTT 502
QY 121 GlyTYRLeuAlaGlnCysThrPheThrYrMetArgSerAsnSerAlaLeuArgValLeu 140
Db 503 GGGAAATTTGCGGAGTGTACATTTCAAAGATGCTTCAATAGTCTTAAGAGATTGG 562
QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTYRThrPheThr 160
Db 563 TTCAGTGGCTACTTCGGCTAAATGACGAATCATCTGTACGCGTGTATTTCACA 622
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTYRLeuAspGln 180
Db 623 TTCAATGAGAGTGAATGTCAGACCTCTTCCATGAGCTATAATTTATTGGACCAA 682
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db 683 GGAAGCCCTGAAATGAATTAATTAATTCATGCACTTCTTCTGCGAAGGACTT 742
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220

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Db 743 TGTGAAGAAATGCGTGAATTAAGTGAATGCTGATCTCGGTTGCACTTGTCAAT 802
QY 221 TYRProLYSGlyAspAlaSerThrGlyTYRAsnSerValSerArgIleIleIleGln 240
Db 803 TACCAAAATGAGATGCTTCTTACGATGAGTAATTCAGTTCTGCAATTAATGAAGA 862
QY 241 LeuProLYS 243
Db 863 CTACCAAAA 871

RESULT 7
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LOCUS
DEFINITION
Pan troglodytes CTRC1 gene, VIRUAL TRANSCRIPT, partial sequence,
AY399085
ACCESSION
AY399085
VERSION
AY399085.1 GI:39755074
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
1 (bases 1 to 732)
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D., and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D., and Cargill,M.
DIRECT SUBMISSION
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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1..732
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="CTRCL"
/locus_tag="HCM0106"
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ORIGIN
Alignment Scores:
Pred. No.: 2.7e-111 Length: 732
Score: 1272.00 Matches: 239
Percent Similarity: 98.35% Conservative: 0
Best Local Similarity: 98.35% Mismatches: 4
Query Match: 97.77% Indels: 0
Gaps: 9
US-10-063-734-122 (1-243) x AY399085 (1-732)
QY 1 MetATGProGlnGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 1 ATGCAACCCCAAGGCGCCCGCCCTCCGCAAGCGGCTCCGCGCTCTGCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGln 40
Db 21 CTGCTGCACTGCGCCCGCCCTGCAAGCGCTCTGCAATCCCAAGGGAAGCAAAAGCG 120
QY 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTYRAsnGlyMetCysLeuGlnGlyProAla 60
Db 121 CAGCTCCCGCAAGGAGGAGGTGGGACCTGTATTAATGAATGGCTTCAAGGCGCAGCA 180

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QY 61 G1yVal1ProG1yARgAspG1ySerProG1yAlaAsnVal11eProG1yThrProG1yIle 80
 DB 181 GGAGTGGCTGCTGACGACGGAGCCCTGGGGCCAAATGCAATTCGGGTACACCTGGGATC 240
 QY 81 ProG1yARgAspG1yPhelYsg1yG1yG1yCysLeuArgG1ySerPheG1yGlu 100
 DB 241 CCAGGTGGGATGATTCAGAGAGAGAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAG 300
 QY 101 SerTPThProAsnTyrlYsg1yCysSerTPSerSerLeuAsnTyrlYleAspLeu 120
 DB 301 TCCTGGACACCCAACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 121 G1yVal1eAlaG1yCysThrPheThrYsMetArgSerAsnSerAlaLeuArgVal1e 140
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 QY 141 PheSerG1ySerLeuArgLeuYsCysArgAsnAlaCysCysG1yNArgTPYrPheThr 160
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 DB 481 TTCAGTGGCTGAG 540
 QY 181 G1ySerProG1yMetAsnSerThr11eAsn11e11eArgThrSerSerValG1yG1yLeu 200
 DB 541 GGAGAGCCCTGAAATGATTCACACATTAATTCATTCGACTTCTTCTGGAGAGACTT 600
 QY 201 CysG1yG1y11eG1yAlaG1yLeuValAspValAla11eTPYrG1yYrCysSerAsp 220
 DB 601 TGTGAAGGATGGTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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 DB 661 TACCCAAAAG 720
 QY 241 LeuProYs 243
 DB 721 CTACCAAAA 729

RESULT 8
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 LOCUS AL544722 Homo sapiens PLACENTRA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION Clome CS0D1022YF04 5-PRIME, mRNA sequence.
 ACCESSION AL544722
 VERSION AL544722.3 GI:45745219
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 827)
 Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:3126563.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?b=CS0D1022D020P1c=4941.f.
 Location/Qualifiers
 1..827
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/mol_type="mRNA"
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 /clone_lib="Homo sapiens PLACENTRA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 9,58e-111 Length: 827
 Score: 1267.00 Matches: 241
 Percent Similarity: 99.18% Conservative: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 97.39% Indels: 1
 DB: Gaps: 0

US-10-063-734-122 (1-243) x AL544722 (1-827)

QY 1 MetArgProG1yG1yProAlaAlaSerProG1yNArgG1yLeuLeuLeuLeu 20
 DB 70 ATGCACCCCAAGGAGCCGCCCTCCCGACGCGCTCCGGGCTCTGCTGCTCTG 129
 QY 21 LeuLeuG1yLeuProAlaProSerSerAlaSerG1y11eProYsg1yYsAla 40
 DB 130 CTGCTGACGCTCCCGCCCGCTGAGCGCTTGAGATCCCAAGGAGAGAGAGAGAG 189
 QY 41 G1yLeuArg1yNArgG1yVal1yAspLeuYrAsnG1yMetCysLeuG1yN1yProAla 60
 DB 190 CAGTC-CGGCAGAGGAG 248
 QY 61 G1yValProG1yARgAspG1ySerProG1yAlaAsnVal11eProG1yThrProG1yIle 80
 DB 249 GGAGTGGCTGCTGACGACGGAGCCCTGGGGCAATGCAATTCGAGTACACCTGGGATC 308
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 DB 309 CCAGGTGGGATGATTCAG 368
 QY 101 SerTPThProAsnTyrlYsg1yCysSerTPSerSerLeuAsnTyrlYleAspLeu 120
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 QY 141 PheSerG1ySerLeuArgLeuYsCysArgAsnAlaCysCysG1yNArgTPYrPheThr 160
 DB 489 TTCAGTGGCTCACTTGGCTAAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
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 DB 549 TTCAGTGGCTGAG 608
 QY 181 G1ySerProG1yMetAsnSerThr11eAsn11e11eArgThrSerSerValG1yG1yLeu 200
 DB 609 GGAGAGCCCTGAAATGATTCACACATTAATTCATTCGACTTCTTCTGGAGAGACTT 668
 QY 201 CysG1yG1y11eG1yAlaG1yLeuValAspValAla11eTPYrG1yYrCysSerAsp 220
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 QY 221 TyrProYsg1yAspAlaSerThrG1yTPAsnSerValSerArg11e11e11eG1yGlu 240
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 QY 241 LeuProYs 243
 DB 789 CTACCAAAA 797

RESULT 9
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LOCUS AL551834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS001061YA20 5-PRIME, mRNA sequence.
ACCESSION AL551834
VERSION AL551834.3 GI:45856624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1100)
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31273650.
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS001061BA100P1ac=4941.f.
FEATURES
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location/Qualifiers
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/clone="CS001061YA20"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1,76e-110 length: 1100
Score: 1266.00 Matches: 241
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 97.31% Indels: 1
Gaps: 0
US-10-063-734-122 (1-243) x AL551834 (1-1100)
QY 1 MetAagProGInGlyProAlaAlaSerProGInaArgLeuArgGlyLeuLeuLeuLeu 20
Db 94 ATGCACCCCGAGGGCCCGCCGCTCCCGCGAGCGGCTCCGGGCTCTGCTGCTCTG 153
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnLeuAla 40
Db 154 CTGCTGCGAGCTGCCCGCCGCTCGAGCCCTCTGAGATCCCAAGGGGAGCAAAAGCG 213
QY 41 GInLeuArgGInaArgGInaValAlaAspLeuTyraGInGlyMetCysLeuGInGlyProAla 60
Db 214 CA-CTCCGGCAGAGGAGAGTGTGAGCTGTATATGAAATGCTTACAAAGGCCAGCA 272
QY 61 GInValProGInaArgAspGlySerProGInaAlaValIleProGInaProGIna 80
Db 273 GGAATGCTGTGTCAGAGAGGAGCCCTGGGGCCATGTCATTCGGGTACACCTGGGATC 332
QY 81 ProGInaArgAspGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 333 CCAAGTGGAGATGATTCAAAGAGAAAGGGGAGAAATGTCGAGGAGAAAGCTTTGAGAG 392

QY 101 SerTrrProAsnTyrlsGInCysSerTrpSerSerLeuAsnTyrlsleapleu 120
Db 393 TCCTGAGACCCCACTACAGAGAGTTCATGAGACTTCATTAATTAAGCATAGACTT 452
QY 121 GInValIleAlaGInCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValleu 140
Db 453 GGAATAATGTCGAGATGATTCATTAACAAAGATGCGTCAATAGTCTTAAGGTTTG 512
QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysGInGInaGTTTrrPheThr 160
Db 513 TTCAGTGGTCACTTCGCGCTAAATGCAATATCAATGCTGTCAGCTGTGATTTTCA 572
QY 161 PheArgGInAlaGInCysSerGlyProLeuProIleGInaIleIleIleIleIleIle 180
Db 573 TTCATGAGAGCTGATGATGTCAGACTCTCCCTTAAGCTATTAATTTTGGACCA 632
QY 181 GlySerProGInaMetAsnSerThrIleAsnIleHisArgThrSerSerValGInGlyLeu 200
Db 633 GGAAGCCTGAAATGAATTCACATTAATTAATTCATGCACTTCTGTGGAGAGACTT 692
QY 201 CysGInGlyIleGInAlaGInLeuValAspValAlaIleTrrValGlyThrCysSerAsp 220
Db 693 TGTGAAGAAATGGATGGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
QY 221 TyrProGlyGInaAspAlaSerThrGlyTrrPAsnSerValSerArgIleIleIleGInGIn 240
Db 753 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 812
QY 241 LeuProIys 243
Db 813 CTACCAAAA 821

RESULT 10
LOCUS BMS60093 1132 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6592628 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5476455
5', mRNA sequence.
ACCESSION BMS60093
VERSION BMS60093.1 GI:18804229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1132)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LMNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LNCM1992 row: 0 column: 16
High quality sequence stop: 638.
location/Qualifiers
1..1132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5476455"
/issue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_41"
/note="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,

FEATURES
source

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

| Pred. No.: | 6,85e-110 | Length: | 1132 |
|------------------------|-----------|---------------|------|
| Score: | 1260.00 | Matches: | 239 |
| Percent Similarity: | 97.95% | Conservative: | 0 |
| Best Local Similarity: | 97.95% | Mismatches: | 4 |
| Query Match: | 96.85% | Indels: | 1 |
| DB: | 4 | Gaps: | 0 |

US-10-063-734-122 (1-243) x BMS60093 (1-1132)

```

Qy 1 MetATGProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeu 20
Db 87 ATGCCAGCCCGAGGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCG 146
Qy 21 LeuLeuGInLeuProAlaProSerSerAlaSerGlu1LeuProGlyGlyGInysAla 40
Db 147 CTGCTGCACTGCCCGCCGCTGAGCGCTCTGAGATCCCGAGGGGAGAGAGAGCG 206
Qy 41 GInLeuArgGInArgGluValAlaLeuLeuTyraGlyMetCysLeuGInGlyProAla 60
Db 207 CAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 266
Qy 61 G1yValProG1yArgAspGlySerProG1yAlaAsnVal1LeuProG1yThrProG1y 80
Db 267 GGAGAGCCCTGCTGAGACCGGAGCCCTGCGGCGCAATGAGATCCCGGCTACCTGGAGATC 326
Qy 81 ProG1yArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 327 CAGGCTCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386
Qy 101 SerTPThrProAsnTyrlsGInGlySerTPSerSerLeuAsnTyrlsGly1LeuAspLeu 120
Db 387 TCCTGGACACCCACATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
Qy 121 G1yVal1LeuAlaG1ySerThrPheThrlyMetArgSerSerSerAlaLeuArgValLeu 140
Db 447 GGGAAATATGCGAGATGATTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
Qy 141 PheSerG1ySerLeuArgLeuTyraGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
Db 507 TTCAGTGGCTCACTTGGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
Qy 161 PheAsnG1yAlaG1yCysSerG1yProLeuPro1LeuAla1Leu1Leu1Leu1Leu1Leu 180
Db 567 TTCATGAGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626
Qy 181 G1ySerProG1yMetAsnSerThr1LeuAsn1Leu1Leu1Leu1Leu1Leu1Leu1Leu 200
Db 627 GGAAGCCCTGATGATTCATTAATGATTCATTCATTCATTCATTCATTCATTCATTCATTC 686
Qy 201 CysGInGly1LeuG1yAlaG1yLeuValAla1Leu1Leu1Leu1Leu1Leu1Leu1Leu 220
Db 687 TGTGAAGGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 746
Qy 220 P1yProG1yG1yAspAlaSerThrG1yTyraSerSerAlaSerArg1Leu1Leu1Leu1Leu 240
Db 747 TTACCAAAAGAGAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 806
Qy 240 uLeuProG1y 243
Db 807 ACTACCCAAA 816

```

RESULT 11
AL532456 1098 bp mRNA linear EST 24-MAR-2004
LOCUS AL532456 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS00M01YN20 5-PRIME, mRNA sequence.
ACCESSION AL532456

VERSION AL532456.3 GI:45707373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1098)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31070288.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4941.f.
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS00M014DG10QPL&c=4941.f.

FEATURES

source

```

1..1098
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS00M014YN20"
/issue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

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ORIGIN

Alignment Scores:

| Pred. No.: | 2,46e-109 | Length: | 1098 |
|------------------------|-----------|---------------|------|
| Score: | 1254.00 | Matches: | 238 |
| Percent Similarity: | 98.35% | Conservative: | 0 |
| Best Local Similarity: | 98.35% | Mismatches: | 4 |
| Query Match: | 96.39% | Indels: | 1 |
| DB: | 1 | Gaps: | 0 |

US-10-063-734-122 (1-243) x AL532456 (1-1098)

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Qy 2 ArgProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeuLeu 21
Db 2 CCCCCCGAGGGCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTGCTG 61
Qy 22 LeuGInLeuProAlaProSerSerAlaSerGlu1LeuProGlyGlyGInysAlaGIn 41
Db 62 CTGCAAGCTCCCGCGCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
Qy 42 LeuATGInArgGluValAlaLeuLeuTyraGlyMetCysLeuGInGlyProAlaGly 61
Db 122 TC-CGCGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 62 ValProG1yArgAspGlySerProG1yAlaAsnVal1LeuProG1yThrProG1y1LeuPro 81
Db 181 GTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 82 G1yArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 101
Db 241 GGTCCGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 102 TTPThrProAsnTyrlsGInGlySerTPSerSerLeuAsnTyrlsGly1LeuAspLeuGly 121
Db 301 TGGACACCCACATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

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QY 122 Lys11ealagluCyThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeuPhe 141
 Db 361 AAAATGCGGAGTGTACATTACAAAGATGCGTTAAATAGGCTCAAGAGTTTGTTC 420
 QY 142 SerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPhe 161
 Db 421 AGTGCTCCTCGCTCGCTAAATGCGAATGCAATGCTGCTGAGCGTTGATTTACATTC 480
 QY 162 AsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGly 181
 Db 481 AATGAGCTGATATTTCAGACCTCTTCCCATTAAGATATATATTTTGGACCAAGA 540
 QY 182 SerProGluMetLeuSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCys 201
 Db 541 AGCCCTAAATGAATTCACAAATTAATATTCATGCACTTCTTGTGGAGAGACTTGT 600
 QY 202 GluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyr 221
 Db 601 GAAAGATTGGTGTGATTAAGTGAATGCTATCTGGGTTGCGACTTGTTCAGATTAC 660
 QY 222 ProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeu 241
 Db 661 CCAAAAGAGATGCTTCTACTGATGATGCAATTCAGTTCTGCACTATTATTGAAGACTA 720
 QY 242 ProLys 243
 Db 721 CCAAAA 726

RESULT 12
 EX387691 986 bp mRNA linear EST 29-APR-2004
 LOCUS BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1037YD19 5-PRIME, mRNA sequence.

ACCESSION BX387691
 VERSION BX387691.2 GI:46875049
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHOR Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30461701.

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas=CS0A1037CB10QPl&c=4941.f.

FEATURES
 source location/Qualifiers
 1..986

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1037YD19"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 7.99e-109 Length: 986

Score: 1248.00 Matches: 238
 Percent Similarity: 97.94% Conservative: 0
 Best Local Similarity: 97.94% Mismatches: 5
 Query Match: 95.93% Indels: 1
 DB: 5 Gaps: 0

US-10-063-734-122 (1-243) x BX387691 (1-986)

QY 1 MetArgProGlnGlyProAlaIleSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 93 ATGCAACCCCAAGAGCCCGCCGCTCCCGCAGCGCTCCGCGCTCCGCTCCG 152
 QY 21 LeuLeuGlnLeuProAlaIleProSerSerAlaSerGluIleProLysGlyLysGlnVal 40
 Db 153 CTGCTGAGCTGCCCGCCGCTCCGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 212
 QY 41 GlnLeuArgGlnArgGlyValValAspLeuTyrArgGlyMetCysLeuGlnGlyProAla 60
 Db 213 CAGTC-CGGCAGAGGAGGTGTGTGACCTGTATATGGAATGTGCTTACAGGCGCAGCA 271
 QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
 Db 272 GGAAGCTGTGTCGAGAGCGGAGCTGGGCGCAATGCAATTCGGGTACCTGGAGATC 331
 QY 81 ProGlyArgAspGlyPheLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 332 CAGGTGCGGATGATTCACAAAGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 391
 QY 101 SerThrProAlaIleGlyGlnCysSerThrSerSerLeuAsnTyrGlyIleAspLeu 120
 Db 392 TCTGGAACACCACTACCAAGAGTGTTCATGAGATTCATTAATATGAGCATATGATCTT 451
 QY 121 GlyIleIlealagluCyThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 452 GGGAAATTCGAGAGTGTATTAACAAGATGCTTCAATATGATGCTTAAGATTTTG 511
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 Db 512 TTGAGTGGCTCATTGGCTTAATACAAATGATGTGTMACGTTGGATTTTCA 571
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
 Db 572 TTCATGAGCTGAATGATTCAGGACTCTTCCCATTTGAAGCATATATTATTGACCA 631
 QY 181 GlySerProGluMetLeuSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
 Db 632 GGAAGCTTAATGAATTCACAAATTAATATTCACACTTCTTGTGGAAGCACTT 691
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPValGlyThrCysSerAsp 220
 Db 692 TGTGAAGGAATGTGCTGATTAAGTGAATGTGTCTATCTGGGTGGCACTGTTCAGAT 751
 QY 221 TyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGlu 240
 Db 752 TACCAAAAGAGAGTCTTACTGATGATGAAATWCAATTTCTCCCATCATTAATGAAGA 811
 QY 241 LeuProLys 243
 Db 812 CTACAAAA 820

RESULT 13
 LOCUS CR592899 710 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CS0D1077YB01 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 ACCESSION CR592899
 VERSION CR592899.1 GI:50473706
 KEYWORDS HTC; cNSUT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 710)

| | |
|--|--|
| AUTHORS | Li, W.B., Gruber, C., Jesse, J. and Poljans, D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished |
| REMARK | Contact : Feng Liang Email : fliang@life-tech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Parade Avenue 2 (bases 1 to 710) |
| REFERENCE | Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1..710 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSOD1077YB01" /tissue.type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6" |
| FEATURES | |
| SOURCE | |
| ORIGIN | |
| Alignment Scores: | |
| Pred. No.: | 6.52e-107 Length: 710 |
| Score: | 1226.00 Matches: 229 |
| Percent Similarity: | 99.57% Conservative: 0 |
| Best Local Similarity: | 99.57% Mismatches: 1 |
| Query Match: | 94.24% Indels: 0 |
| DB: | 3 Gaps: 0 |
| US-10-063-734-122 (1-243) x CR592899 (1-710) | |
| Oy | 14 ArgGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuProAlaProSerSeraLaseGluile 33 |
| Dd | 3 CGGGGCTTCCTGCTCTCTCTGCTGCTGACGCTGCCGCCCTCGAGCCCTCTTGAGATC 62 |
| Oy | 34 ProlysglyLylysglnylnylnylnylnylnylnylnylnylnylnylnylnylnylny 53 |
| Dd | 63 CCAAGGGGAAGCAAAAGGCCGAGCTCCGGCGAGAGAGAGTGCTGAGCCTGTATATGTA 122 |
| Oy | 54 MetCysLeuGlnGlnGlyProAlaGlyValProGlyA-gaspGlySerProGlyAlaasnVal 73 |
| Dd | 123 ATGTGCTTAAACAAGGGCCACAGAGAGTGCTGTGTCAAGCGGAGCCCTGGGGCCCAATGCC 182 |
| Oy | 74 IleProGlyLThrProGlyYlleProGlyLArgAspGlyPheIysGlyGluIysGlyGlyCys 93 |
| Dd | 183 ATTCGGGGATCACTGGGATCCAGAGTCGGGATGGATTCAAAGAGAAAAGGGGAGATGT 242 |
| Oy | 94 LeuArgGlySerPheGlnGlyLysSerTrpThrProAsnYrlyGlnCysSerTrpSerSer 113 |
| Dd | 243 CTGAGGGAAGAGCTTTGAGAGAGTCTTGACACCAACCACTAACAGAGTTTCATGAGATTCA 302 |
| Oy | 114 LeuAsnYrGlyYlleAspLeuGlylylylleAlaGluCysThrPheThrIlySmetArgSer 133 |
| Dd | 303 TTGATTATTTGGATATGATCTTGGGAAAATTTGGGAGGTGTACATTTACAAAGATGCGTTCA 362 |
| Oy | 134 AsnSerAlaLeuArgValLeuPheSerGlySerLeuArgGlyLeuIysCysArgSmaIaCys 153 |
| Dd | 363 AATAGTGTCTTAAGAGTTTGTGTTCAGTGGCTCACTTCGGCTAAATGCGAAGATGCATGC 422 |
| Oy | 154 CysGlnArgTrpYrPheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGlu 173 |
| Dd | 423 TGTCAAGCGTGGTATTTTCATCATTTAGAGAGCTGATGATTTTCAGACCTCTTCCATTTGAA 482 |
| Oy | 174 AlaIleIleIyYrLeuAspGlnGlySerProGlyMetAsnSerThrIleAsnIleHisArg 193 |
| Dd | 483 GCTAATATTTATTTTGACCAAGAGAGCCCTGAAATGAATTCACATTAATATTCATTCGC 542 |

| | | | |
|--|---|--|-----------------------------|
| QY | 19 | Thrserservalglunglyleucyagglnglyllecylalaglyleuvalaspvalalalle | 213 |
| Db | 543 | ACTCTCTGTGGAGGACCTTTGTGAAGCAATTGGCTGCATTATGTCGATCTCTATC | 602 |
| QY | 214 | TrpValglYthrCyssersasPLY-ProlysglyAspalaaserthglYTrpAsnserVal | 233 |
| Db | 603 | TGGTGTGGTACTGTTGTCAGATTACCAAAAGAGATGCTTCTACTGATGAGATTCACTT | 662 |
| QY | 234 | SerArgllellellelleglugluLeuProlys | 243 |
| Db | 663 | TCTGCATCATATTATGGAAGACTACCAAA | 692 |
| RESULT 14 | | | |
| LOCUS | CB201936 | 849 bp | mRNA linear EST 05-FEB-2005 |
| DEFINITION | AGENCOURT 11289616 NIH_MGC135 Mus musculus cDNA clone | | |
| ACCESSION | IMAGE:30140382 5', mRNA sequence. | | |
| VERSION | CB201936 | | |
| KEYWORDS | CB201936.1 GI:28236469 | | |
| SOURCE | EST. | | |
| ORGANISM | Mus musculus (house mouse) | | |
| REFERENCE | Mus musculus | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| JOURNAL | Unpublished (1999) | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cga@bgs-remail.nih.gov Tissue Procurement: Dr. David Rowe cDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: NDAM0046 row: f column: 07 High quality sequence stop: 710. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..849 | | |
| | /organism="Mus musculus" | | |
| | /mol_type="mRNA" | | |
| | /db_xref="taxon:10090" | | |
| | /clone="IMAGE:30140382" | | |
| | /lab_host="DH10B (phage-resistant)" | | |
| | /clone_id="NIH_MGC_135" | | |
| | /note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GCTAGTGTCTAGATCGGAGCGGCGCC(T)3' Tissue contributed by, David Rowe. Library constructed by Resgen, Invitrogen Corp." | | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. NO.: | 5,46e-105 | Length: | 849 |
| Score: | 1207.00 | Matches: | 229 |
| Percent Similarity: | 95.10% | Conservative: | 4 |
| Best Local Similarity: | 93.47% | Mismatches: | 10 |
| Query Match: | 92.77% | Indels: | 2 |
| DB: | 6 | Gaps: | 1 |
| US-10-063-734-122 (1-243) x CB201936 (1-849) | | | |
| QY | 1 | MeLrAgpGpGInGlypProAlAlAserProGInArgLeuArgGly-----LeuLeu | 18 |
| Db | 41 | ATGACACCCCAAGGACCGGCGGCCCCCGGAGCGTGGCTGGGCTCTCTTCCTTGGCTG | 100 |

QY 19 LeuleuLeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLysGlyLysGln 38
 Db 101 CTGCTGCTGTACAGTTGTCGCCACCGTCCAGCGCTCTGAGAACCCCAAGCTAGACAA 160
 QY 39 LysAlaGlnLeuArgGlnArgGlnValValAlaAspLeuTyrAsnGlyMetCysLeuGlnGly 58
 Db 161 AAAGCGCTGATCCCGCAGAGGAGAGGTGTAGACCTGTATATATGAAATGTCTACAGGA 220
 QY 59 ProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTyrPro 78
 Db 221 CCACAGAGAGTTCCCGGTCGTGATGGAGCCCTGGGCGCAAGCGCATTCCTGGCACACT 280
 QY 79 GlyIleProGlyArgAspGlyPheLysGlyGlyLysGlyLysGlyLysGlyLysGlyPhe 98
 Db 281 GGCATCCAGGTCCGAGTGTGATTCAAAGGGGAAAGGAGAAATGCTTAAGGAAAGCTTT 340
 QY 99 GluGluSerTrpTrpProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyTyr 118
 Db 341 GAGAGTCTCTGAGACCCCAAACTATATACAGTGTCTGGAGTGTCTGAACTATAGCATTA 400
 QY 119 AspLeuGlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
 Db 401 GATCTTGGGAAATATGGAGAGTGTACATTCACGAAATGGCTCCCAAGTCTCTGCGA 460
 QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyr 158
 Db 461 GTTCTGTTCAGTGTCTGCTGCTGCTCAATGCAAGATGCAATGCTGTGACCGCTGTAT 520
 QY 159 PheThrPheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrIleu 178
 Db 521 TTATACATTTATGAGAGTGAATGTTCAGACCTCTTCCATCCAGACCATCATCATATG 580
 QY 179 AspGlnGlySerProGlnLysMetAsnSerThrIleAsnIleHisArgThrSerSerValGln 198
 Db 581 GACCAAGAGAGCCCTGATTAATCACTATTAATCAATCAATCAATCAATCAATCAATCA 640
 QY 199 GlyLeuCysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleThrValGlyThrCys 218
 Db 641 GGACTCTGTGAGAGGAGTGTGTGTGATGTGTGATGTGTGATGTGTGATGTGTGATGT 700
 QY 219 SerAspTyrProLysGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIle 238
 Db 701 TCAGATTATCCCAAGAGAGAGCGCTCTCTACATGATGATGATGATGATGATGATGAT 760
 QY 239 GluGluLeuProLys 243
 Db 761 GAAAAAATCTCCGAAA 775

RESULT 15
 AV399086
 LOCUS
 DEFINITION Mus musculus CTHRC1 gene, VIRUTAL TRANSCRIPT, partial sequence,
 ACCESSION AV399086
 VERSION AV399086.1 GI:39755075
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 738)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,D.J.,

TITLE
 JOURNAL
 COMMENT
 FEATURES
 source
 gene
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,02e-105 Length: 738
 Score: 1205.00 Matches: 229
 Percent Similarity: 94.69% Conservative: 3
 Best Local Similarity: 93.47% Mismatches: 11
 Query Match: 92.62% Indels: 2
 Gaps: 1
 US-10-063-734-122 (1-243) x AV399086 (1-738)
 QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----Leuleu 18
 Db 1 ATGACCCCAAGGCCCCCGCGGCCCCCGACACTGCTGCTGCTCTCTCTGCTGCTG 60
 QY 19 LeuleuLeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLysGlyLysGln 38
 Db 61 CTGCTGCTGTACAGTTGTCGCCACCGATTCAGAGGCTCTGAGAACCCCAAGGTGAGCAA 120
 QY 39 LysAlaGlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGly 58
 Db 121 AAAGCGCTGATCCCGCAGAGGAGGTGTAGACCTGTATATATGAAATGTCTACAGGA 180
 QY 59 ProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTyrPro 78
 Db 181 CCACAGAGAGTTCCCGGTCGTGATGGAGCCCTGGGCGCAAGCGCATTCCTGGCACACT 240
 QY 79 GlyIleProGlyArgAspGlyPheLysGlyGlyLysGlyLysGlyLysGlyLysGlyPhe 98
 Db 241 GGCATCCAGGTCCGAGTGTGATTCAGAGGAGAAAGAGAAATGCTTAAGGAAAGCTTT 300
 QY 99 GluGluSerTrpTrpProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyTyr 118
 Db 301 GAGAGTCTCTGAGACCCCAAACTATATACAGTGTGTGTGATGCTGATGCTGATGCTG 360
 QY 119 AspLeuGlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
 Db 361 GATCTTGGGAAATATGGAGAGTGTACATTCAGAGAGAGCGCTCCCAAGTCTCTGCGA 420
 QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyr 158
 Db 421 GTTCTGTTCAGTGTCTGCTGCTGCTCAATGCAAGATGATGATGATGATGATGATGAT 480
 QY 159 PheThrPheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeu 178
 Db 481 TTATACATTTATGAGAGTGAATGTTCAGACCTCTTCCACAGAAAGCATCATCTATCTG 540
 QY 179 AspGlnGlySerProGlnLysMetAsnSerThrIleAsnIleHisArgThrSerSerValGln 198
 Db 541 GACCAAGAGAGCCCTGAGTGAATTAATCACTATTAATTAATTAATTAATTAATTAATTA 600
 QY 199 GlyLeuCysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleThrValGlyThrCys 218
 Db 601 GGCATCTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 219 SerAspTyrProLysGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIle 238
 Db 661 TCAGATTATCCCAAGAGAGAGCGCTTCTACATGATGATGATGATGATGATGATGATGAT 720

| Db | 721 | GAAGAACTACCGAA | 735 |
|------------|---|----------------|------------------------|
| RESULT 16 | | | |
| LOCUS | AK003674 | 1161 bp | mRNA |
| DEFINITION | AK003674 | | linear HTC 03-APR-2004 |
| ACCESSION | AK003674 | | |
| VERSION | AK003674.1 | | GI:12833485 |
| KEYWORDS | HTC; CAP trapper. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | 1 | | |
| AUTHORS | Carninci, P. and Hayashizaki, Y. | | |
| TITLE | High-efficiency full-length cDNA cloning | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | |
| MEDLINE | 99279253 | | |
| PUBMED | 10349636 | | |
| REFERENCE | 2 | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | | |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | | |
| MEDLINE | 20499374 | | |
| PUBMED | 11042159 | | |
| REFERENCE | 3 | | |
| AUTHORS | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Teshiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, T., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format | | |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) | | |
| MEDLINE | 20530913 | | |
| PUBMED | 11076661 | | |
| REFERENCE | 4 | | |
| AUTHORS | The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | |
| JOURNAL | Nature 409, 685-690 (2001) | | |
| MEDLINE | 5 | | |
| PUBMED | | | |
| REFERENCE | | | |
| AUTHORS | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | | |
| TITLE | Analysis of the mouse transcriptome based on functional annotation | | |
| JOURNAL | of 60,770 full-length cDNAs | | |
| MEDLINE | Nature 420, 563-573 (2002) | | |
| PUBMED | 6 (bases 1 to 1161) | | |
| REFERENCE | | | |
| AUTHORS | Adachi, J., Aizawa, K., Akabira, S., Akimura, T., Arai, A., Aono, H., Arkawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasaoka, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, I., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (10-JUN-2000) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group RIKEN Genomic Sciences Center (GSC), | | |

RIKEN Yokohama Institute; 1-7-22 Suehico-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsic.riken.jp, URL: <http://genome.gsic.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsic.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGGAGAGAGGCGCGGACACTCGAGTCTTTTATTTTATTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGGAGAGAGAGATCCAGAGCTCAATTATTTATTAACCCCCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end; SstI, 3' end; XhoI. Host: SOLR.

Location/Qualifiers

1..1161

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:1110014B07"

/db_xref="taxon:10090"

/clone="1110014B07"

/issue_type="whole body"

/clone_id="RIKEN full-length enriched mouse cDNA library"

/dev_stage="18-day embryo"

69..806

/note="unnamed protein product; hypothetical collagen triple helix repeat containing protein (InterPro|IPR00087, evidence: InterPro) putative"

/codon_start=1

/protein_id="BAB2930.1"

/db_xref="GI:12834486"

/translation="MHPQRAAPRQILLGLFVLILLQLSAPISASBNPKYKQALLI RORVVDLYNMCLOGPAGVRGDSGANCIPTPTPIPRDQKSGKEGLRSPFEE SMTPEYKQCSMSLNYGIDLGKIAETFTMRSSARLVFSGSLRKRNAACORWYMFTEFGACSGPLPLEAIIYLDQSGPELNTINIHRTSSVGLCEGIGAGLVDAIMWG TCSDPYKGDASITGMNSVSRRIIEBLPK"

1141..1146

/note="putative"

1161

/note="putative"

ORIGIN

polyA_signal

polyA_site

Alignment Scores:

Prod. No.:

Score: 1201.00

Percent Similarity: 94.69%

Best local Similarity: 93.06%

Query Match: 92.31%

DB: 3

Gaps: 1

US-10-063-734-122 (1-243) x AK003674 (1-1161)

Qy 1 MetArgrProGngnglyProAlaAlaSerProGlnArghLeuArngly-----LeuLeuLeu 18

Db 69 ATGACACCCCAAGGCGCGGCGCCCCCGGACGCTGCTGGATCTCTTCTTGTCGTG 128

Qy 19 LeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProLygLyGln 38

Db 129 CTGCTGCTGCTACAGTTGTCCGCACGCATACAGCGCTCTGAGAACCCCAAGGTGAGCAA 188

Qy 39 LysAlaGlnLeuArgrGlnArghGlnValAlaAspLeuTyrsnglyMetCysLeuGlnGly 58

Db 189 CAACCGCTGATCCCGCAGAGGAGAGGTGTGACCTGTATATGAGAAATGTCTTCAAGGA 248

Qy 59 ProAlaGlyValProGlyIArgArnglySerProGlyAlaAsnValIleProGlyTyhPro 78

Db 249 CCAGCAGAGAGTTCCCGGTCGTGAAGGAGCCCTGGGCAACGGCAATTCCTGGACACACT 308

QY 79 GlyIleProGlyYArGAspGlyPheIysGlyGlyIuIysGlyGlyCysLeuArgGluSerPhe 98
Db 309 GGATCCAGCTCGGATCGATTCAGAAAGGAGAAAGGAGATGCTTAAGGGAAGCTTT 368
QY 99 GluGluSerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIle 118
Db 369 GAGAGATCTGTGAG 428
QY 119 AspleuGlyIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArg 138
Db 429 GATTTGGGAAATTTGGGAGGTGACATTCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 488
QY 139 ValIeuPheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpTyr 158
Db 489 GTTCTGTTCAGTGGCTCGCTTCGCTCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
QY 159 PheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeu 178
Db 549 TTACATTATATGAG 608
QY 179 AspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlu 198
Db 609 GACCAAG 668
QY 199 GlyLeuGlyGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCys 218
Db 669 GGAAGTCTGTGAG 728
QY 219 SerAspTyrProIysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIle 238
Db 729 TCAGATTACCCCAAG 788
QY 239 GluGluLeuProIys 243
Db 789 GAAGAACTACCGAAA 803

RESULT 17
CA413294/c 716 bp mRNA linear EST 07-NOV-2002
LOCUS UI-H-EZ0-bap-h-20-0-UI.s1 NCI CGAP Ch1 Homo sapiens cDNA clone
DEFINITION UI-H-EZ0-bap-h-20-0-UI 3', mRNA sequence.
ACCESSION CA413294
VERSION CA413294.1 GI:24775945
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 716)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes
FEATURES
source location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ0-bap-h-20-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP Ch1"
/note="Organ: Left Pelvis; Vector: pUT3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pUT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TAGTACGCT.
TAG_TISUB=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTATATGC"

ALIGNMENT SCORES:

Pred. No.: 6.1e-104 Length: 716
Score: 1195.00 Matches: 222
Percent Similarity: 99.11% Conservative: 0
Best Local Similarity: 99.11% Mismatches: 2
Query Match: 91.85% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x CA413294 (1-716)

QY 20 LeuIeuGluGlnLeuProAlaProSerSerAlaSerGluIleProIysGlyIysGlnIys 39
Db 714 CTGCTGCTGAGAGCTGCCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
QY 40 AlaGlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnIlePro 59
Db 654 GCGAGCTCCGCGAG 595
QY 60 AlaGlyValProGlyAlaGagGlySerProGlyAlaAsnValIleProGlyThrProGly 79
Db 594 GCAAGAGTGGCTGTGTCAG 535
QY 80 IleProGlyYArGAspGlyPheIysGlyGlyIuIysGlyGlyCysLeuArgGluSerPhe 99
Db 534 ATCCAGAGTGGAGATGATTCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
QY 100 GluSerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAsp 119
Db 474 GAGTCCCTGGACACCCCAACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
QY 120 LeuGlyIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgVal 139
Db 414 CTGGGAAATTTGGAG 355
QY 140 LeuPheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpTyrPhe 159
Db 354 TTGTCAGTGGCTCACTTGGGCTAAATGCAAAATGATGATGATGATGATGATGATGATGAT 295
QY 160 ThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAsp 179
Db 294 ACAATTCAATGAG 235
QY 180 GlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGly 199
Db 234 CAAG 175
QY 200 LeuGlyGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSer 219
Db 174 CTTTGGAAG 115
QY 220 AspTyrProIysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlu 239

| Db | 114 | GATTAACCCAAAGGANGCTTTCATCGTAGGAAATTCAGTTTCGCATCATTTATGA | 55 |
|------------|---|--|-----------------------------|
| Oy | 240 | GlutenPolyr 243 | |
| Db | 54 | GACTACCCAAA 43 | |
| RESULT 18 | | | |
| LOCUS | AK076498 | 1168 bp | mRNA linear HTC 03-APR-2004 |
| DEFINITION | Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833429011 product: hypothetical Collagen triple helix repeat containing protein, full insert sequence. | | |
| ACCESSION | AK076498 | | |
| VERSION | AK076498.1 | GI:26096845 | |
| KEYWORDS | HTC; CAP trapper. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| REFERENCE | 1 | Carninci, P. and Hayashizaki, Y. | |
| AUTHORS | High-efficiency full-length cDNA cloning | | |
| TITLE | Meth. Enzymol. 303, 19-44 (1999) | | |
| JOURNAL | 99279253 | | |
| MEDLINE | 10349636 | | |
| PUBMED | 2 | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | |
| REFERENCE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | |
| AUTHORS | Genome Res. 10 (10), 1617-1630 (2000) | | |
| TITLE | 3 | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuwa, T., Teshiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahigashi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| JOURNAL | RIKEN integrated sequence analysis (RISA) system--384-format | | |
| MEDLINE | sequencing pipeline with 384 multicapillary sequencer | | |
| PUBMED | Genome Res. 10 (11), 1757-1771 (2000) | | |
| REFERENCE | 11076861 | | |
| AUTHORS | 4 | The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | |
| JOURNAL | Nature 409, 685-690 (2001) | | |
| MEDLINE | 5 | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | |
| PUBMED | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs | | |
| REFERENCE | Nature 420, 563-573 (2002) | | |
| AUTHORS | 6 (bases 1 to 1168) | | |
| TITLE | Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mura, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akehira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. | | |
| REFERENCE | Direct Submission | | |
| AUTHORS | Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome | | |

COMMENT

EXPLORATION Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
 Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp,
 URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9222,
 Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Please visit our web site for further details.
 URL: <http://genome.gsc.riken.jp/>
 URL: <http://fantom.gsc.riken.jp/>.
 Location/Qualifiers

FEATURES

Source

1..1168

/organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="PANTOM:DB:4833429011"
 /db_xref="taxon:10090"
 /clone="4833429011"
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 /clone_lib="RIKEN full-length enriched mouse cDNA library
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 containing protein (InterPro|IPR000087, evidence:
 InterPro)
 putative"
 1148..1153
 /note="putative"
 1168
 /note="putative"

ORIGIN

Alignment Scores:

Pred. NO.:

Score: 2.58e-102 Length: 1168

Percent Similarity: 1181.00 Matches: 226

Best local Similarity: 93.90% Conservative: 5

Query Match: 91.87% Mismatches: 12

Query Match: 90.78% Indels: 3

DB: 3 Gaps: 1

US-10-063-734-122 (1-243) x AK076498 (1-1168)

QY 1 MetArpProGInGlyProAlaAlaSerProGInArGLeuArGly-----LeuLeuLeu 18

DB 76 ATGCACCCCCCAAGGCCGGCGCCCCCCCCGACGCTGCTCGTCTCTTCTTGCTG 135

QY 19 LeuLeuLeuLeuGInLeuProAlaProSerSerAlaSerGInuileProLyGslYpGIn 38

DB 136 CTGCTGCTGCTACAGTTGTTCGCACCCATCATGCGCCTCTGAGAACCCCAAGGTGAAGCA 195

QY 39 LysAlaGInLeuArGInArGInuAlaValAspLeuTYraGInGlyMetCysLeuGInGly 58

DB 196 AAACGGCTGATCCGCGACGAGAGAGGTGTATACCTGTATATGGAATGTGCTTACAAGGA 255

QY 59 ProAlaGlyValProGInArGAspGlySerProGlyAlaAanValIleProGlyThrPro 78

DB 256 CCACACGAGAGTCCCGGTCGTGAATGGAGGCCCTGGGGCAACGGCATTCCTGGCACACT 315

QY 79 GlyIleProGlyArGAspGlyPheIysGslYgInuYsgIyGluCyLeuArGsluSerPhe 98

DB 316 GGCATCCCAAGTTCGGAGATGGAATTCAAGAGGGAAGAGAGATGTTTAAGGAAAGCTTT 375

QY 99 GluGluSerThrPThrProAenTYrIysGInCysSerTPSerSerLeuAsnTYrGlyIle 118

DB 376 GAGGAGTCTTGAGACCCCAACTAATAGACAGTGTTCGTGAATTCCTGAACATATGACATA 435

QY 119 AspLeuGlyIysIleAlaGluCyThrPheThrIysMetArgSerAanSerAlaLeuArg 138

DB 436 GATCTGGGAAATATTCGGAAGTGTATCATTCAGAAAGATGGCGCTCCAAACATGCTCTGGCA 495

QY 139 ValLeuPheSerGlySerLeuArgLeuYsCyArgAsnAlaCyCysGlnArgTrpTyr 158
 Db 496 GTTCGTTCAAGGCTCCGCTCGCTCAATGACAGAAATGATGTCACCGCTGAT 555
 QY 159 PheThrPheAsnGlyAlaGluCysSerGlyPro-LeuProIleGluAlaIleIleTyrLe 178
 Db 556 TTTCATTATTAATGAGATGGAATGTCAGACCTTCTCCAGAGACATCATATCT 615
 QY 178 uAsGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValG 198
 Db 616 GGACCAAGAGAGCCCTGATTAATCACTATTAAATTCATCGTACTCTCTGGA 675
 QY 198 uGlyLeuCySerGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCy 218
 Db 676 AGGACTCTGGAAGGATAGGTGCTGATGTTGTTGATGTCCTGCTGCTGCTGCTG 735
 QY 218 sSerAspTrpProGlySerGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIle 238
 Db 736 TTTCGATTACCCCAAGAGAGAGCGCTTCTACTGATGAAATTCGTCGTCATCATCT 795
 QY 238 eGluGluLeuProlys 243
 Db 796 TGAAGACTACCGAA 811
 RESULT 19
 AL553798 709 bp mRNA linear EST 30-MAR-2004
 LOCUS AL553798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSOD1077YB01 5-PRIME, mRNA sequence.
 ACCESSION AL553798
 VERSION AL553798.3 GI:45858563
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 709)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:1275612.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnafre=CSOD1077CA01QPI&c=4941.f.
 FEATURES
 source location/Qualifiers
 1..709
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1077YB01"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 6.14e-102 Length: 709
 Score: 1174.00 Matches: 223
 Percent Similarity: 97.38% Conservative: 0
 Best Local Similarity: 97.38% Mismatches: 6
 Query Match: 90.24% Indels: 1

DB: 1 Gaps: 0
 US-10-063-734-122 (1-243) x AL553798 (1-709)
 QY 15 GlyLeuLeuLeuLeuLeuLeuLeuLeuProAlaProSerSerAlaSerGluIlePro 34
 Db 6 GGATTCCTGCT 65
 QY 35 LysGlyLysGlnLysAlaGlnLeuArgGlnArgGlnValValAlaPheLeuTyrAsnGlyMet 54
 Db 66 AAGGGAGACCAAGAGCCCA-CTCCGAGAGAGGAGGTGTGACCTGTATTAATGGAATG 124
 QY 55 CysLeuGlnGlyProAlaGlyValProGlyYArgAspGlySerProGlyAlaAsnValIle 74
 Db 125 TCGTTCAAGAGGCCAGCAGAGAGTGGTCTGTGACCGGAGCCCTGGGCGCAATGCAAT 184
 QY 75 ProGlyThrProGlyIleProGlyYArgAspGlyPheLysGlyLysGlyGlyCysLeu 94
 Db 185 CCGGGTACACCTGGAGATCCAGTCCGGAGATGATTCMAAGAGAAAGGGGNAATGCTG 244
 QY 95 ArgGluSerPheGluGluGluSerTrpThrProAsnTyrLysGlnCysSerTrpSerLeu 114
 Db 245 AGGAAAGCTTTGAGAGTCTGAGACCCAACTCAAGAGAGTTCATGAGATTCATG 304
 QY 115 AsnTyrGlyIleAspLeuGlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsn 134
 Db 305 AATTATGGCAATGATCTTGGGAAATTCGCGAGATGATTCATTACAAAGATGCTCAAT 364
 QY 135 SerAlaLeuArgValLeuPheSerGlySerLeuArgLeuYsCyArgAsnAlaCyCys 154
 Db 365 AGTGTCTAAGAGTTTGTTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 424
 QY 155 GlnArgTrpTyrPheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAla 174
 Db 425 CAGGTGTGGAATTCACATTCATGAGATGATGTTGACGACCTCTCCATTCAGACT 484
 QY 175 IleIleTyrLeuAspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThr 194
 Db 485 ATATTTATTTGACCAAGAGAGCCCTGAAATGAATTCACAAATTAATTCATGCGACT 544
 QY 195 SerSerValGlnGlyLeuCySerGlyIleGlyAlaGlyLeuValAspValAlaIleTrp 214
 Db 545 TCTTCTGTGAGAGACTTGTGTGAAGATTTGGTGGATTAAGTTCATGCTCTCTCTCT 604
 QY 215 ValGlyThrCysSerAspTrpProGlySerGlyAspAlaSerThrGlyTyrAsnSerValSer 234
 Db 605 GTTGGTACTGTTCACATTAACCAAGAGAGTCTTCTACTGATGATGAATTTCTTA 664
 QY 235 ArgIleIleIleGluGluLeuProlys 243
 Db 665 CGCATCATTTATTCAGAACCTTACCAAAA 691
 RESULT 20
 BX386416 707 bp mRNA linear EST 27-APR-2004
 LOCUS BX386416 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSOD1077YB01 5-PRIME, mRNA sequence.
 ACCESSION BX386416
 VERSION BX386416.2 GI:46627527
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 707)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 8, 2003 this sequence version replaced gi:30457424.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalised. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1941.f

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?S=CS1A1020ZB01QP1&c=4941.f>.

FEATURES

SOURCE

```

1. 707
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSOD1077B01"
/tissue_type="P16CENTA.COT 25-NORMALIZED"
/clone_id="Homo sapiens P16CENTA.COT 25-NORMALIZED"
primer="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMSPORT 6 vector. Library was normalized."

```

ORIGIN

| | |
|--|-----------------|
| Alignment Scores: | |
| Pred. No.: | 5.6e-100 |
| Score: | 1153.50 |
| Percent Similarity: | 97.82% |
| Best Local Similarity: | 97.82% |
| Query Match: | 88.66% |
| DB: | 5 |
| US-10-063-734-122 (1-243) x BX386416 (1-707) | |
| | Length: 707 |
| | Matches: 224 |
| | Conservative: 0 |
| | Mismatches: 5 |
| | Indels: 2 |
| | Gaps: 0 |

US-10-063-734-122 (1-243) x BX386416 (1-707)

| | | | |
|----|-----|--|-----|
| Oy | 15 | G VleuLeuLeuLeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGlnIlePro | 34 |
| Db | 6 | GGATTCCTGCTGCTCTGCTGCTGCAGCTGCCCGCCGCGTGCAGGGCGCTTCGAATCCCC | 65 |
| Oy | 35 | LySGIYLvSGInLysAlaGlnLeuAArgGlnAArgIuValAlaSpLeuTyPAsnGlyMet | 54 |
| Db | 66 | AAAGGGAAGCAAAAGGCGC--sTCCGGCAGAGGAGGTGGATGACCTGTATATAGGATG | 123 |
| Oy | 55 | CyLeuGlnGlyProAlaGlyValPProGlyAArgaArgIySerProGlyValaAsnValIle | 74 |
| Db | 124 | TGCTTAAAGGGCCACAGAGAGCTCTGTATCAGACGGAGGCCCTGGGGCCAAATGGCATT | 183 |
| Oy | 75 | ProGlyThreProGlyIlePProGlyAArgaArgIyPheLySGIYLvLysGlyGlyCysLeu | 94 |
| Db | 184 | CCGGGATCACTCGGATCCCAAGTCCGAGTCCGAGTTCAGATTCAGAGGAAAGGGGAATGTCTG | 243 |
| Oy | 95 | ArgGlnSerPheGlnGlnGlnSerTTrpThrProAsnTyLysGlnCysSerTTrpSerSerLeu | 114 |
| Db | 244 | AGGGAAGACTTTAGAGAGTCTCTGCACACCCAACTCAAGCAAGTGTTCATGGAGTTCAATG | 303 |
| Oy | 115 | AsnTyPArgIyLleAspLeuGlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsn | 133 |
| Db | 304 | AAATTAATGGCAATATATCTTGGAAATATGGGAGGTGATCACTTTAAACAAATATCGTTCAAT | 363 |
| Oy | 135 | SerAlaLeuArgValLeuPheSerSerGlySerLeuAArgLeuLysCysArgAsnAlaCysCys | 154 |
| Db | 364 | AGTGTCTTAGAGATTTTGTTCAGTGGCTCACTTCGGCTAAATGCAAGAAATGCATGCTGT | 423 |
| Oy | 155 | GlnArgTrpTyPThrPheThrPheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAla | 174 |
| Db | 424 | CAGGTTGATTTTCACTTCATTCATGAGCTGATGTTTCAGAGCTCTTCCCATTTGAAGCT | 483 |
| Oy | 175 | IleIleIyPLeuAspGlnGlySerProGlnMetAsnSerThrIleAsnIleHisArgThr | 194 |
| Db | 484 | ATAATTTATTTGAGCAACAGAGACCCCTGAAATGAATTCACAAATTAATTAATTCATGCACCT | 543 |
| Oy | 195 | SerSerValGlnGlyLeuLeuCysGlnGlyIleGlyAlaGlyLysValAspValAlaIleTrp | 214 |
| Db | 544 | TCTTCTGTGAGAGCACTTGTGTAGAGAAATTTGTGTGCAATTGTTGTGATGTTCCTATCTGG | 603 |
| Oy | 215 | ValGlyThrCysSerAspTyPProLySGlyAspAlaSerThrGlyTTrpAsnSerValSer | 234 |

| | | | |
|----|-----|--|-----|
| D6 | 604 | GTGGGACTGTTTCACATTA-CCAAAGAGATGCTTCTACTGCATGGAATTCAGTTCT | 662 |
| QY | 235 | ArgIleIleIleGluGluLeuProIys | 243 |
| D6 | 663 | CGCATCATTTATGAGAACTACCAAAA | 689 |

RESULT 21

| | | | | | |
|------------|---|-------------|------|--------|-----------------|
| LOCUS | B1108785 | 790 bp | mRNA | linear | EST 26-JUN-2001 |
| DEFINITION | 602089527F01 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:5024946 5' , , , | | | | |
| ACCESSION | mRNA sequence. | | | | |
| VERSION | B1108785 | | | | |
| KEYWORDS | B1108785.1 | GI:14559686 | | | |
| SOURCE | ESF. | | | | |
| ORGANISM | Mus musculus (house mouse) | | | | |
| | Mus musculus | | | | |
| | Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. | | | | |
| REFERENCE | 1 (bases 1 to 790) | | | | |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/ . | | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| JOURNAL | Unpublished (1999) | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. | | | | |

FEATURES

Source

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5024946"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT
library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

```

ORIGIN

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 3,79e-99 |
| Score: | 1145.50 |
| Percent Similarity: | 93.06% |
| Best Local Similarity: | 91.43% |
| Query Match: | 88.05% |
| DB: | 4 |
| | |
| Length: | 760 |
| Matches: | 224 |
| Conservative: | 4 |
| Mismatches: | 9 |
| Indels: | 8 |
| Gaps: | 3 |

US-10-063-734-122 (1-243) X BI108785 (1-790)

```

Oy 2 AisProGlnGly1ProAlaIaIaSerProGlnAaGlyuAaGGlyY-----LeuLeuLeuLeu 19
Oy 10 :::::-----CGAGAGCGAGCGCTCGGATCTCTTCTCTTGCTGCTG 60
Db 10 AGGCGCGGCGGCGCC-----CGAGAGCGAGCGCTCGGATCTCTTCTCTTGCTGCTG 60

Oy 20 LeuLeuLeuGlnLeuProAlaIaProSerSerAlaSerGluIleProIyGlyIyGlnLys 39
Db 61 CTGTGTCTAAGTGTTCGCGACCGATACAGCGGCTCTTGAGAACCCCGAGGTAGAGCAAAAA 120

Oy 40 AlaGlnLeuAaGlnAaGlnGluValAlaIaIaLeuTyTyAaGlnTyMetCysLeuGlnGlyPro 59
Oy 121 GCCTGATCTCCGAGAGGAGGTGTGTAGACCTGTATATATGTGAATGTGTCTTACAGAGCA 180
Db 121

```


| SOURCE ORGANISM | REFERENCE AUTHORS | TITLE | JOURNAL COMMENT |
|----------------------|---|---|-----------------|
| Homo sapiens (human) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | 1 (bases 1 to 671) | |
| | NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap . | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), | |
| | Tumor Gene Index | Unpublished (1997) | |
| | Contact: Robert Strausberg, Ph.D. | Email: cgapbs-remail.nih.gov | |
| | Tissue Procurement: James Martin | CNA Library Preparation: Dr. M. Bento Soares, University of Iowa | |
| | DNA Sequencing by: Dr. M. Bento Soares, University of Iowa | Clone Distribution: Clone distribution information can be obtained | |
| | from Dr. M. Bento Soares, bento-soares@iowa.edu | The following repetitive elements were found in this CNA | |
| | sequence: 1-28, >AT-rich#low_complexity | Seq primer: M13 FORWARD | |
| | POLYA=yes. | | |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .671 |

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UT-H-FG1-bgk-c-06-0-UT"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FG1"
/notes="Organ: Enchondroma; Vector: pRTT3-Pac (Pharmacia)
with a modified polylinker. Site_1: EcoR I, Site_2: Not I;
NCI CGAP FG1 is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pRTT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_LIB=UT-H-FG1
TAG_SEQ=CGGTCACTC"

```

| ORIGIN | |
|--|----------|
| Alignment Scores: | |
| Pred. No.: | 1.98e-98 |
| Score: | 1137.00 |
| Percent Similarity: | 99.06% |
| Best Local Similarity: | 99.06% |
| Query Match: | 87.39% |
| DB: | 5 |
| US-10-065-734-122 (1-243) x BU624465 (1-671) | |
| Length: | 671 |
| Matches: | 210 |
| Conservative: | 0 |
| Mismatches: | 2 |
| Indels: | 0 |
| Gaps: | 0 |

| | | | |
|----|-----|--|-----|
| QY | 32 | GIuIleProLysGlyLyseGlnLysAlaGlnLeuArgGlnLysGluValValAspLeuTyr | 51 |
| DB | 671 | GAGATCTCCCAAGNAGACAAAGGCGCAGCTCCGCGAGAGAGAGGTGTGACCTTAT | 612 |
| QY | 52 | AaNgIyMeLcysLeuGlnGlyProAlaGlyValProGlyIArgAspGlySerProGlyVala | 71 |
| DB | 611 | AATGGAATGTGCTTACAAAGGCGCAGCAGAGTGTCTGTGAGACGGGAGCCCTCGGGGCC | 552 |
| QY | 72 | AaValIleProGlyThrProGlyIleProGlyIArgAspGlyPheLysGlyGluLysGly | 91 |
| DB | 551 | AATGGCATTCGGGATCACCTGGGATTCACAGTTCGGATGATTCAAGAGAGAAAGGGG | 492 |

[illegible]

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
Email: seqr@genoscope.cns.fr, [Web : www.genoscope.cns.fr](http://www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers
 enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by ligo technology, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.F
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cnats=CS0DI077CAO1NP1fc=4941.f>.
Location/Qualifiers

```

source
1..676
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CGSD1077YB01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```


| | | | |
|----|-----|--|-----|
| Db | 663 | GGAGGCCCTGAATGAAATTCAACAACTTAATATTCATCGCACTTCCTCTGTGGAGAGACT | 722 |
| Qy | 200 | uCyGlu-GlyTllegIyAla-GlyLeuValAspValAla-IleTrp-ValGlyThrCys | 219 |
| Db | 723 | TTGGAAAGGAATGGTGCTCGGATTAATGATGTGGCTATCTGGGGTTGGCACTGTT | 782 |
| Qy | 219 | erAspIyrProLyseIyAspAlaSerThrngIyTrpAnsSerValSerArg----- | 235 |
| Db | 783 | TCCAATTACCCCAAAAGGAGATGCTTTCTTACTGGAGGAAATTCAGTTTTTCGCCCA | 842 |
| Qy | 236 | --IleIleIleGluIuLeuProLys | 243 |
| Db | 843 | TCATTATTTTGGAGAACTACCCCAA | 868 |

CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM2007 row: n column: 21
 High quality sequence stop: 482.
 Location/Qualifiers

FEATURES

1. 1037
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5482196"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_41"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2,95e-95 Length: 1037
 Score: 1106.50 Matches: 219
 Percent Similarity: 94.44% Conservative: 2
 Best Local Similarity: 93.59% Mismatches: 8
 Query Match: 85.05% Indels: 5
 DB: 4 Gaps: 1

US-10-063-734-122 (1-243) x BW915926 (1-1037)

QY 1 MetAtpProGlnG1yProAlaIaSerProGlnAArgLyuLeuLeuLeu 20
 Db 86 ATGCCAAGCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTG 145
 QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGluLeuProLyG1yLysGlnLysAla 40
 Db 146 CTGCTGCAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGCAAAAGCG 205
 QY 41 GlnLeuAArgGlnAArgGluValAlaAspLeuLyTrasnGlyMetCysLeuGlnGlyProAla 60
 Db 206 CAGCTCCGCGCAGGAGGAGGTGTGAGCCTGTATTAATGGAATGTCTTACAGGGCCACGA 265
 QY 61 G1yValProG1yAArgSPG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
 Db 266 GAGAGTGGCTGGTGCAGAGAGGAGCCCTGGGGCCATTCGAGTACACCTGGGATC 325
 QY 81 ProG1yAArgSPG1yPheLySG1yGluLySG1yGluCysLeuAArgLyuSerPheGluGlu 100
 Db 326 CCAAGTCCGAGATGATTCAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGAG 385
 QY 101 SerTrpThrProAsnTrpLySG1yCysSerTrpSerSerLeuAsnTrpLyIleAspLeu 120
 Db 386 TCCCGACACCACTACACAGAGTGTCTGAGAGTTCATTAAGATTAATGAGATGATCTT 445
 QY 121 G1yLyS1leAlaGluCysTrhPheThrLySMeArSerArSerArSerAlaLeuAArgValLeu 140
 Db 446 GGGAAATTCGGGAGTGTACATTACAAAGATGGCTTAATGTCTTAAAGATTTC 505
 QY 141 PheSerG1ySerLeuAArgLeuLyCysAArgAsnAlaCysCysGlnAArgTrpLyPheThr 160
 Db 506 TTCAATGAGCTACTTCGGCTAAATGCAACAATGACATGCTGTGAGCTGGTATTTCACG 565
 QY 161 PheAsnG1yAlaGluCysSerG1yProLeuAArgProIleGluAlaIleIleLyTrLeuAsnGln 180
 Db 566 TTCAATGAGAGCTGAATGTTCAGAGACCTCTTCCCATTTAAGCTAATAATTATTGGACCA 625

QY 181 GlySerPro-GluMetAsnSerThrIleAsnIleHisArg-ThrSerSerValGluGlyL 200
 Db 626 CGAAGCCCTCGAAGAAATGAATTCACATATGATTCATCGGAGACTTCTCTGTGAAAGAC 685
 QY 200 euCyGluGluGlyIleGlyValAlaGlyLeuValAlaIleTrpVal-GlyThrCysSe 219
 Db 686 TTTCGAGAGAAATGTGTCTGATTAAGAGATGTGTATTCGAGGCTTGAGACTTGTTC 745
 QY 219 rAspTrpProLySG1yAspAlaSerThrGlyTrp 230
 Db 746 ACATTAACCCCAAGGAATGCTTCACCC---TGG 776

RESULT 28
 BQ425266
 LOCUS
 DEFINITION
 AGENCOURT 7912803 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150166
 5', mRNA sequence.
 ACCESSION
 BQ425266
 VERSION
 BQ425266.1 GI:21120581
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC <http://mgs.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strauberg, Ph.D.
 Email: cgaubs-ri@mail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM13484 row: f column: 23
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES

SOURCE

1. 851
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6150166"
 /tissue_type="amelanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 3.14e-95 Length: 851
 Score: 1105.00 Matches: 216
 Percent Similarity: 95.61% Conservative: 2
 Best Local Similarity: 94.74% Mismatches: 6
 Query Match: 84.93% Indels: 4
 DB: 5 Gaps: 2

US-10-063-734-122 (1-243) x BQ425266 (1-851)

QY 1 MetAtpProGlnG1yProAlaIaSerProGlnAArgLyuLeuLeuLeu 20
 Db 168 ATGCCAAGCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTG 227
 QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGluLeuProLyG1yLysGlnLysAla 40
 Db 228 CTGCTGCAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGCAAAAGCG 287
 QY 41 GlnLeuAArgGlnAArgGluValAlaAspLeuLyTrasnGlyMetCysLeuGlnGlyProAla 60

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Db 288 CAGCTCCGCGCAGAGGAGGTGGACCTGTATTAATGATGCTTACAGAGGCCAGCA 347
Qy 61 G1yValProG1yAArgAspG1ySerProG1yAlaAsnVal11leProG1yThrProG1yIle 80
Db 348 GGAAGTCCCTGGTCTGAGACCGGAGCCCTGGGGCCAAATGGCATTCGGGTACACCTGGGAAC 407
Qy 81 ProG1yAArgAspG1yPhe1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 100
Db 408 CCAAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 467
Qy 101 Ser1yPThrProAsn1yR1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 120
Db 468 TCCTGGACACCCACACACACACACACACACACACACACACACACACACACACACACACAC 527
Qy 121 G1y1yG1y1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 140
Db 528 GGGAAATATGCGAGAGTACATTTACAAAGATGCCCTTCAAAATGATGCTTAAAGAGTTTG 587
Qy 141 PheSerG1ySer1yLeuArg1yLeu1ySer1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 160
Db 588 TTCAGTGGCTCACTTCTGGCTAAATGCAAGAAATGATGCTGTCAGCGTGGATTTTCAACA 647
Qy 161 PheAsnG1yAlaG1yCysSerG1yProLeuPro1yG1yAla1yIle1yIle1yIle1yIle 180
Db 648 TTCATGAGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATATTTATTGGACCAA 707
Qy 181 G1ySerProG1yLeuMeAsnSerThr1yIleAsn1yIleHis1yArg1ySer1yVal1yG1yLeu 200
Db 708 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGACCTCTCTGGAAGAGACAT 767
Qy 201 CysG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 219
Db 768 TGTGAAAGAAATTTGCTGCTGAATTAATGAGATGTTGCTATCTGGGGGATGGACATGGT 827
Qy 219 erAsp---TyrPro1yG1y 224
Db 828 TCAGATTTACCAAAAGG 847

RESULT 29
AL575307 1102 bp mRNA linear EST 06-APR-2004
LOCUS AL575307 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1061YA20 3-PRIME, mRNA sequence.
ACCESSION AL575307
VERSION AL575307.3 GI:46248266
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1102)
L1,W.B., Gruber,C., Jessee,J. and Polyes,D.
Full-length cDNA libraries and normalization.
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31313615.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1061B1A10NP1c=4941.f.
FEATURES
source
1..1102
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

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/clone="CS0D1061YA20"
/issue_type="PLACENTA COR 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COR 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5,55e-95 Length: 1102
Score: 1104.00 Matches: 219
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 91.25% Mismatches: 16
Query Match: 84.86% Indels: 6
DB: 1 Gaps: 2

US-10-063-734-122 (1-243) x AL575307 (1-1102)
Qy 4 G1yG1yProAla1yAla1ySerProG1yAArg1yLeu1yLeu1yLeu1yLeu1yLeu1yLeu 23
Db 1075 CAGGCCCCS---CSCCTCCCGCAGCGGCGCG-----CTTCTGCTTT-CTGYRS 1029
Qy 24 LeuProAlaProSerSer1yAlaSerG1yLeu1yPro1yG1yG1yG1yG1yG1yG1yG1yG1y 43
Db 1028 TGCAGTGGCCCGCGCGCTCGCGCTTATGATCCCAAGGAGCAAAAGCCGACGCTCCGG 969
Qy 44 G1yAArg1yVal1yAla1ySer1yLeu1yArg1yMetCys1yG1yG1yG1yG1yG1yG1yG1y 63
Db 968 CAGAGGAGGTGGT-GACCTGTATATGAAATGCTTCAACAGGGCCAGCAGAGAGTGGCT 910
Qy 64 G1yAArgAspG1ySerProG1yAlaAsnVal1yIleProG1yThrProG1yIleProG1yArg 83
Db 909 GGTCCAGAGAGGAGCCCTGGGGCCAAATGCAATTCGGGTACCTCGGATCCCAAGTCCG 850
Qy 84 AspG1yPhe1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1y 103
Db 849 GATGATTTCAAGAGAGAAAGGGAGATGCTGAGGGAAGCTTTGAGAGATCTTGAGACA 790
Qy 104 ProAsn1yR1yG1yCysSer1yPThrSer1yLeuAsn1yR1yG1yIleAsp1yG1yIle 123
Db 789 CCCAATCTCAACAGCAGTTCATGAGATTCATGAATTAATGATGATCTTGGGAAATTT 730
Qy 124 AlaG1yCysThrPheThr1yMet1yArgSer1yAsn1yAla1yArg1yVal1yLeuPheSerG1y 143
Db 729 GCGAGGTGACTTTCACAAAGATGCTCAATATGATGCTTAAAGATTTGTTCACTGAG 670
Qy 144 Ser1yLeuArg1yLeu1yCysArg1yAsn1yAlaCysCysG1yArg1yR1yPThrPheAsnG1y 163
Db 669 TCACCTTCGGCTAAATGAGAGAAATGCAATGCTGTCAAGCGTGGTATTTACATTCATGAGA 610
Qy 164 AlaG1yCysSerG1yProLeuPro1yG1yAla1yIle1yIle1yIle1yIle1yIle1yIle 183
Db 609 GCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTTAATTAATTTATTTGACCAAGAGCCCT 550
Qy 184 G1yMet1yAsn1yThr1yIleAsn1yIleHis1yArg1yR1ySer1yVal1yG1yLeu1yCysG1y 203
Db 549 GAAATGAATTCACAAATTAATTAATTCATGCACTTCTCTGAGAGAGACTTGTGAAGGA 490
Qy 204 I1yG1yAlaG1yLeu1yVal1yAsp1yVal1yAla1yIle1yR1yPThr1yCysSer1yR1yPThr 223
Db 489 ATTTGCTGCGATTTGATGATTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 430
Qy 224 G1yAsp1yAla1ySer1yThr1yPhe1ySer1yVal1ySer1yG1yIle1yIle1yG1yG1yLeu1y 243
Db 429 GGAAGATGCTTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370

RESULT 30
AL564395 1064 bp mRNA linear EST 05-APR-2004
LOCUS AL564395 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0D0014YN20 3-PRIME, mRNA sequence.
ACCESSION AL564395
```

VERSION ALS64395.3 GI:46231315
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1064)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31288373.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 This sequence belongs to sequence cluster 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0DM014DG10NP1&c=4941.f.
 location/Qualifiers

FEATURES
 source
 1..1064
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM014YN20"
 /issue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 5,97e-94 Length: 1064
 Score: 1093.00 Matches: 221
 Percent Similarity: 91.32% Conservative: 0
 Best Local Similarity: 91.32% Mismatches: 17
 Query Match: 84.01% Indels: 8
 DB: 1 Gaps: 2
 US-10-063-734-122 (1-243) x ALS64395 (1-1064)

QY 3 ProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 22
 Db 1064 CCCCAGGCCCC---CSCYCCCCCGAGGGYCGGCC-----CTCTTGTG-CTCTTCTGT 1015
 QY 23 GlnLeuProAlaProSerSerAlaSerGluLeuLeuLeuLeuLeuLeu 42
 Db 1014 GCAGCTCCCGCGCGGTGAGGCTTT-GAGATCCCA-GGGAAGCAAAAGCCAGCTC 957
 QY 43 ArgGlnArgGluValAlaAspLeuTyArgGlyLeuLeuLeuLeuLeuLeu 62
 Db 956 CGGAGAGGAGGAGT-GTGGACCTGTATATGATGCTTACAAAGGCGCAGGAGTG 898
 QY 63 ProGlnArgArgGlySerProGlyAlaAsnValLeuProGlyThrProGlyLeuProGly 82
 Db 897 CTTGTGTGAAGCGGAGCCCTCGGCGCAATGCAATCCGGGTACACCTGGGATCCCAAGT 838
 QY 83 ArgAspGlyPheLeuGlyGluGlyGluGluGluGluGluGluGluGluGlu 102
 Db 837 CGGGATGATTCAGAGAGAAAGGGGAAATGCTTGAGGAAAGCTTTGAGGAGTCTCTGG 778
 QY 103 ThrProAsnTyrlsGlnGlySerTyrSerSerLeuAsnTyrlsGlyLeuAspLeuGly 122
 Db 777 ACACCCCACTACAAGCAGTGTTCATGAGTTCAATGATTAATGCAATGATTTGGGAAA 718

QY 123 IleAlaGluCysThrPheThrIysSerArgSerAsnSerAlaLeuArgValLeuPheSer 142
 Db 717 ATGGGAGAGTGTACATTTTACAGATGCTTCAATATGCTCTTCAAGATTTTGTAAAGT 658
 QY 143 GlySerLeuArg-LeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAs 162
 Db 657 GGCTCACTTCGGCGGCAAAATGCAAAATGCAATGCTGTGACGGTTGGATTCATTCA 598
 QY 162 nGlyAlaGluCysSerGlyProLeuProGluGluAlaIleIleTyrLeuAspGlnGly 182
 Db 597 TGGAGCTGAATGTTGAGACCTCTTCCATGAAAGCTATATATTATTGGACCAAGAG 538
 QY 182 ProGluMetAsnSerThrIleAsnIleHISArgThrSerSerValGluGlyLeuGly 202
 Db 537 CCTCAAAATGAAATCAACAATATATATTCATCGACTCTTCTGTGAGAGCATTTGTCA 478
 QY 202 nGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPvalGlyThrCysSerAspTyr 222
 Db 477 AGGATTTGCTGTGATTAAGATGATGCTATCTGGTGGCAGCTGTTCAGATTACCC 418
 QY 222 OlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeuPr 242
 Db 417 AAAAGAGATGCTCTTCTACTGAGATGGAATTGATGCTCTCCATCATTTATTAAGAACTACC 358
 QY 242 OlyG 243
 Db 357 AAAA 354

RESULT 31
 BM915288 1099 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT 6702310 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481457
 DEFINITION BM915288 5' mRNA sequence.
 ACCESSION BM915288
 VERSION BM915288.1 GI:19365667
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1099)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLN at:
 http://image.jnl.gov
 Plate: L1CM2005 row: p column: 02
 High quality sequence start: 26
 High quality sequence stop: 565.
 Location/Qualifiers

FEATURES
 source

1..1099
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5481457"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 41"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

| Pred. No.: | 1.55e-90 | Length: | 1099. |
|------------------------|----------|---------------|-------|
| Score: | 1057.50 | Matches: | 212 |
| Percent Similarity: | 92.80% | Conservative: | 7 |
| Best Local Similarity: | 89.83% | Mismatches: | 8 |
| Query Match: | 81.28% | Indels: | 9 |
| | | Gaps: | 2 |

US-10-063-734-122 (1-243) x BM915288 (1-1099)

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QY 1 MetatgProglnglyProAlaIaaserProglnglyLeuleuLeuleu 20
Db 99 ATGCCAGCCCAAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCCG
QY 21 LeuleuLeuProAlaProSerSerAlaSerGluIleProlysglylyVala 40
Db 159 CTGCTGCAAGCTCCCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGGCGG 218
QY 41 GlnLeuAArgGlnArgGluValAlaAspleuTyraSgLMetCyLeuGlnGlyProAla 60
Db 219 CAGCTCCGCGCAGAGGAGGTGGAGCTGTATATGAGATGCTTACAAAGGCGCAGA 278
QY 61 GlyValProGlyAArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 279 GGAAGTCCCTGCTCGAGACCGGAGCCCTGGGCGCAATGGCATTCGGGTCACCTGGGATC 338
QY 81 ProGlyAArgAspGlyPheIlysglylyGlyGlyCysLeuAArgGlySerPheGlyGlu 100
Db 339 CAGAGTCGGAGTGAATTCAAAGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 398
QY 101 SerTPThrProAsnTyrllysglyCysSerTPSerSerLeuAsnTyrllyIleAspleu 120
Db 399 TCCTGACACCCCAACTACAGAGAGTGTATGATGATGATGATGATGATGATGATGATGAT 458
QY 121 GlyValIleAlaGlyCysThrPheThrIlyMetAArgSerAAsnSerAlaLeuAArgValleu 140
Db 459 GGGAAATTTGGCGAGTGCATTACAAAGATCCGTTCAAAATGATGCTTAAAGATTTTG 518
QY 141 PheSerGlySerLeuAArgLeuIlyCysAArgAsnAlaCysCysGlnAArgTPTrPheThr 160
Db 519 TTCAGAGGCTCACTTCGCTAAATATGAGAAATGATGATGATGATGATGATGATGATGAT 578
QY 161 PheAArgIlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleIleTyrlleuAspGln 180
Db 579 TTCACATGAGAGTGAATGTTCAAGACCTCTCCATTGAAGCTATATATTATTTGACCAT 638
QY 181 -GlySerProGlyMetAArgSerThrIleAsnIleHisArg-ThrSerSerValGluGly 200
Db 639 AGAAACCCCTGAATGATGATTCACAACTTAAATTTCTCCCAACTTTCTTGGGGAGAGAC 698
QY 200 euCysGluGlyIleGlyAlaGlyLeuVal-AspValAlaIleTrp-----ValGly 216
Db 699 TTTTGCAAGAAATGGCGCTGATTAATGAGATGTTGCTATCGGGGTTGGCAACTGGT 758
QY 217 ThrCysSerAspTyrlProlysglyAep-AlaSerThrGly 229
Db 759 -----TCAATTAACCAAAAGGGAATGCTTCCACAGG 792

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RESULT 32
 LOCUS BQ574527 617 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-H-E21-dba-e-10-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone
 UI-H-E21-dba-e-10-0-UI 3', mRNA sequence.
 ACCESSION BQ574527
 VERSION BQ574527.1 GI:21477837
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 617)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapb-rt@mail.nih.gov
 Tissue Procurement: Dr. Steven Gilelis/ Rush Presbyterian, Dept. of
 Orthopaedics

CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-28, >AT rich#low_complexity
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1..617
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E21-dba-e-10-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch2"
 /note="Organ: Left Pelvis; Vector: pRTT3-Pac (Pharmacia)
 with a modified polylinker; Site 1: Ecor I; Site 2: Not I;
 NCI CGAP Ch2 is a normalized cDNA library containing the
 following tissue(s): Chondrosarcoma Grade II. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an Ecor I
 adaptor, digested with Not I, and cloned directionally
 into pRTT3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TGATCAGCT.
 TAG TISSUE=grade-2-chondrosarcoma
 TAG LIB=UI-H-E21
 TAG_SEQ=ATCTAATATG"

ORIGIN

Alignment Scores:

| Pred. No.: | 1.57e-88 | Length: | 617 |
|------------------------|---|---------------|-----|
| Score: | 1033.00 <td>Matches:</td> <td>191 </td> | Matches: | 191 |
| Percent Similarity: | 98.45% <td>Conservative:</td> <td>0 </td> | Conservative: | 0 |
| Best Local Similarity: | 98.45% <td>Mismatches:</td> <td>2 </td> | Mismatches: | 2 |
| Query Match: | 79.40% <td>Indels:</td> <td>1 </td> | Indels: | 1 |
| | | Gaps: | 0 |

US-10-063-734-122 (1-243) x BQ574527 (1-617)

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QY 51 TYraAnglyMetCyLeuGlnGlyProAlaGlyValProGlyAArgAspGlySerProGly 70
Db 616 TATATATGAAATGCTTACCAAGGCGCAGAGAGTGGCTGGTGAAGCGGAGCCCTGGG 557
QY 71 AlaAsnValIleProGlyThrProGlyIleProGlyAArgAspGlyPheIlysglylyVala 90
Db 556 GCCAATGGCATTCGCGGATCACCTGGAGATCCAGATGGAGATGATTCAAAGAGAGAAAG 497
QY 91 GlyIlyCysLeuAArgGlySerPheGlyGluGlySerTPTrProAsnTyrllysglyCysSer 110
Db 496 GGGGAATGCTGAGGGAAGCTTTGAGGAGCTCTGAGACCCCACTCAAGACAGTCTCA 437
QY 111 TPTrSerSerLeuAArgTyrllyIleAspleuGlylyIleAlaGlyCysThrPheThrIly 130
Db 436 TGGAGTTCAATGAATTAATGAGCATGATCTTGGGAAATTTGCGAGATGATCAATTTCAAG 377
QY 131 MetAArgSerAAsnSerAlaLeuAArgValleuPheSerGlySerLeuAArgLeuIlyCysArg 150

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Db 376 ATGGCTCAATATAGCTCTAAGAGTTTGTTCAGTGGCTACTTCGGCTAAATGAGA 317
 Qy 151 AAmIaAcysGslngIaGTrpTyRphethrPheanGlaIaGluCySserGlyProIeu 170
 Db 316 AATGCAATGCTGAGCGTGTGATTTTCATTCATGAGAGTGAATGTTGAGAGCTCTT 257
 Qy 171 ProIleGluAlaIleIleTyRleuAspGlnGlySerProGluMetAnserThrIleAsn 190
 Db 256 CCATTAGAGCTATATTTATTTTGGACCAAGAAAGCCCTGAAATTCACACATTAAT 197
 Qy 191 ILehIaRgThrSerSerValGluGlyLeuCySgluGlyIleGlyAlaGlyLeuValAsp 210
 Db 196 ATTCATCGCACTTCTCTGTGAGAGACTTGTGAGAGATTTGCTGCTGATTTAGTGCAT 137
 Qy 211 ValAlaIleThrValGlyThrCySserAspTyRProLyGlyAspAlaSerThrGlyTr 230
 Db 136 GTTGCCTATCGGTTGGCTGCTGTTCAGATTACCCAAAAGAGATGCTTCTACTGGATG 77
 Qy 230 PaenSerValSerArgIleIleIleGluGluLeuProLyS 243
 Db 76 GAATTCAGTTTCTCGCATCATTTATTAAGAACCTAACCCAA 37

RESULT 33
 B0648112 986 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT_8507019 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297812
 DEFINITION 5', mRNA sequence.
 ACCESSION B0648112
 VERSION B0648112.1 GI:21772284
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1CM2507 row: n column: 21
 High quality sequence stop: 520.
 FEATURES
 source 1..986
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6297812"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_100"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.9kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN
 Alignment Scores:
 Pred. No.:
 Score:

5,79e-87 Length: 986
 1019.50 Matches: 208

Percent Similarity: 88.33%
 Best Local Similarity: 86.67%
 Query Match: 78.35%
 DB: 5
 Gaps: 3

US-10-063-734-122 (1-243) x B0648112 (1-986)

Qy 1 MetArProGlnGlyProAlaIleSerProGlnArgIleuLeuLeuLeu 20
 Db 102 ATGCACCCCGAGGCGCCCGCTCCCGAGCGGCTCCGCGCTCTGCTCTG 161
 Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLyGlyLeuGlnVala 40
 Db 162 CTGCTGCACTGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 221
 Qy 41 GlnLeuArGgIaArGgIaValaIleLeuIleLeuIleLeuIleLeuIleProIa 60
 Db 222 CAGCTCCGCGAGAGAGAGGTGTGACCTGTATTAAGAAATGTCTTACAGGCGCAGCA 281
 Qy 61 GlyValProGlyArGAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 282 GAGTGCCTGTGCGAGCGGAGCCCTGGGCGCAATCGCATTCGGGTACCTGGAGAT 341
 Qy 81 ProGlyArGAspGlyPheLyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 342 CCAAGTGGAGTGTATTCAGAGAAAGAGGAGGAGATCTGAGGGAAGCTTTGAGGAG 401
 Qy 101 SerTrpThrProAntyRlyGlnCySserTrpSerLeuAnthyGlyIleAspLeu 120
 Db 402 TCTTGACACCCACCACTACAGAGTGTCTATGAGTTCATTAAATTAATGCAATGATCTT 461
 Qy 121 GlyIleIleAlaGluCyThrPheThrIleMetArGSerAnSerAlaLeuArGValleu 140
 Db 462 GGGAAATTCGAGAGGTATCAATTAAGAGATGCTTCAATAGTCTTAAGAGATTTT 521
 Qy 141 PheSerGlySerLeuArgLeuLyCySArGAsnAlaCySgluArgTrpTyRphethr 160
 Db 522 TTGAGTGTGCATCTTGGCTTAATATCAAAATGATGCTGACAGCTGTGATTTTCA 581
 Qy 161 PheanGlyAlaGluCySserGlyProIleuProIleGluAlaIleIleTyRleuAspGln 180
 Db 582 TTCAATGAGCTAAATGTTACAGACCTCTCCATTGAAGCTATATTATTTGACCA 641
 Qy 181 GlySerProGluMetAnserThrIleAnIleHisArgThrSerSerVal---GluGly 199
 Db 642 CGAAGCCTGAATGATTCACAAATATATTTCTCCGCACTTCTGTGTGGAAAGA 701
 Qy 199 yLeuCySgluGlyIleGlyAlaGlyLeuValaIleIleIle---TrpValGly--- 216
 Db 702 CTTTGTGAAGAAATGGGGCTGGAATTAATGATGTGCTTATCCTGGGATTTGGGCAC 761
 Qy 217 ThrCySerSerAspTyRProLyGlyAspAlaSerThrGlyTrpPaenSerValSer 234
 Db 762 TTGCTTCAGAAATTAACCCAAAGAAAGATGCTTCTACTGGAATGAAATTTCA 815
 RESULT 34
 AL585129 890 bp mRNA linear EST 28-FEB-2001
 LOCUS ROS019808, mRNA sequence.
 DEFINITION ROS019808, mRNA sequence.
 ACCESSION AL585129
 VERSION AL585129.1 GI:13163862
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 890)
 AUTHORS Murray, F.
 TITLE BP Chicken Embryo Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray

compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., EMAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

| Pred. No.: | 1-71e-82 | Length: | 681 |
|------------------------|----------|---------------|-----|
| Score: | 970.50 | Matches: | 183 |
| Percent Similarity: | 88.55% | Conservative: | 18 |
| Best Local Similarity: | 80.62% | Mismatches: | 22 |
| Query Match: | 74.60% | Indels: | 4 |
| DB: | 5 | Gaps: | 2 |

US-10-063-734-122 (1-243) x BU278868 (1-681)

```

QY 4 GlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeuGln 23
DB 7 CGAGAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
QY 24 LeuProAlaProSerSerAlaSerGluLeuLeuLeuLeuLeuLeuLeuLeu 43
DB 67 CTG-----CGCTCGGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 117
QY 44 GlnArgGlnValValAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 63
DB 118 CCGCGGAGGTGTCTGTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
QY 64 GlyArgAspGlySerProGlnAlaAsnValIleProGlyThrProGlyLeu 83
DB 178 GGAACGGAGCGGAGAACCTTGGAAACCAACGGGATCCCGGAGACCGGGGATCC 237
QY 84 AspGlyPheLeuGlyGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 103
DB 238 GACGGGCGCCAAAGGGGAAAGGGCGAGTCTTGGCGGAGAGCATTTAGAGTCT 297
QY 104 ProAsnTyrLeuGlnCysSerTyrPheSerSerLeuAsnTyrGlyIleAsp 123
DB 298 CCCAATTCAACAGTCTGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 357
QY 124 AlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 143
DB 358 GCGGATGTACCTTCAAAAGATGCGCTCAACAGTCTTCAAGTCTTTCAGTGA 417
QY 144 SerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 163
DB 418 TCGCTCGGCGTGAAGTGGAGGCGGCTGCTGAGCGCTGCTGCTGCTGCTGCT 477
QY 164 AlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 183
DB 478 GCAGAAATCGCGCGGCGCACTTCCCATCAAGCCATTAATTTATGATCAAGG 537
QY 184 GluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 203
DB 538 GAACCTGAACCTTACTATCAATCAACCGAATCTCTCAGTGAAGTCTGTGGAAG 597
QY 204 IleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 223
DB 598 ATCAACGCTGGCTTGTGTGACATCGCATCTGTGAGGACTTGTGATCAACCC 657
QY 223 GgLYAspAlaSerThrGly 229
DB 658 GGGCGATGCTTCTACTGGG 676

```

RESULT 39
LOCUS CB959810
DEFINITION CB959810
ACCESSION CB959810
VERSION CB959810.1 GI:30215926

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 798)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM384 row: h column: 13
High quality sequence stop: 496.
Location/Qualifiers
1. 798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30345876"
/tissue_type="Human Placenta"
/lab_host="DH10B TONa"
/clone_id="NIH MGC 147"
/note="Organ: placenta; Vector: pBluescriptR, Site 1: all-XhoI; Site 2: BamH; Oligo-dT primed using primer insert size 2.3 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH-MGC library."

FEATURES
source

Alignment Scores:

| Pred. No.: | 2.12e-82 | Length: | 798 |
|------------------------|----------|---------------|-----|
| Score: | 970.50 | Matches: | 196 |
| Percent Similarity: | 83.97% | Conservative: | 3 |
| Best Local Similarity: | 82.70% | Mismatches: | 13 |
| Query Match: | 74.60% | Indels: | 25 |
| DB: | 6 | Gaps: | 3 |

US-10-063-734-122 (1-243) x CB959810 (1-798)

```

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 98 ATCCGACCCCAAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 157
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuLeuLeuLeuLeu 40
DB 158 CTGCTGCGAGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGln 60
DB 218 CAGCTCCGCGCAGAGGAGGTGTGACTGTATATGAAATGTGCTTACAAAGG 277
QY 61 GlyValProGlyArgAspGlySerProGlyValAlaAsnValIleProGlyThr 80
DB 278 GGAATGCTGTGTGAGACGGAAGCTTGGGCGCAATGCACTTCCGGTACCTGG 337
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 338 CCAAGTCTGGATGATTCAAAGGAGAAAGGGGAAATGTCTGAGGAAAGCTTTG 397
QY 101 SerTyrProAsnTyrLeuGlnCysSerTyrPheSerSerLeuAsnTyrGlyIle 120

```


Pred. No.: 1,886-80 Length: 995
 Score: 951.50 Matches: 192
 Percent Similarity: 80.23% Conservative: 15
 Best Local Similarity: 74.42% Mismatches: 17
 Query Match: 73.14% Indels: 37
 DB: 5 Gaps: 2

US-10-063-734-122 (1-243) x BU141753 (1-995)

QY 19 LeuLeuLeuLeuLeuLeuProAlaProSerSerAlaSerGluIleProlysglylysgln 38
 DB 14 CTGCTGCTCTCTGCGCCCTGCTGCTGGGCTGCGGCTCCGACAGCCGCGGCGCAAAACAG 73
 QY 39 LysAlaGlnLeuArgGlnArgGlnValAlaAspLeu----- 50
 DB 74 CGAGCG--CGCGCGCGCGGAGGTCTGAGGC-GGTCTGTTTCTCTCTCGAACA 129
 QY 50 ----- 50
 DB 130 TTTTCTCACTCATCTGGAAGCATTAGCTTCCACTGCTCTGCGGCTTCACTT 189
 QY 51 -----TyrAnsglyMetCysLeuGlnGlyProAlaGlyValProGlyArg 65
 DB 130 GAGCACTGCTCTGACAGTACAAAGCGGCTGCTGCTGACAGGCGCCAGCGCGCTCCGCGACCG 249
 QY 66 AspGlySerProGlyValAlaAsnValIleProGlyIleProGlyIleProGlyArgAspGly 85
 DB 250 GACGGGAACCTCGAACCACACCG-GATCCCGGACACCGGAGATCCCGGCGCGGACGCG 308
 QY 86 PheLysGlyGlnLysGlyGlyCysLeuAArgGlySerPheGlyGlySerTrpThrProAsn 105
 DB 309 CCCAAAGGGGAAAGGCGCAAGTCTTCCGCGGAGAGCATTTAGAGAGTCTGAGACGCCAAC 368
 QY 106 TyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeuGlyLysIleAlaGln 125
 DB 369 TTCAGACAGTCTCGTGGAGAGCGACTGACATAGCGCATAGACTGGGAAATAGCGGAA 428
 QY 126 CysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeu 145
 DB 429 TGTAGCTTACAAAGATGGCTTCCACACATGCTCTCAGAGTCTTTTTCAGTGGATGCTC 488
 QY 146 ArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrpPheThrPheAnsglyAlaGln 165
 DB 489 CGGCTGAAAGTCCGAAAGCGCTCTCTCAGCGCTGTACTTCACTTCAATGAGAGAGA 548
 QY 166 CysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGlyMet 185
 DB 549 TCGCGCGGCGCACTTCCCATCGAAGCATTAATATTAGATCAAGGAGTCCGGAAC 608
 QY 186 AsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeuGlySerGlyIleGly 205
 DB 609 AACTCTACTATCAACATACACCGAACCTCTCAGTGAAGTCTTGTTGAAGGAGATCAAC 668
 QY 206 AlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAspTrpProlysglyAsp 225
 DB 669 GCTGGCTTGTGACATCCCATCTGGGTGCGGACTTGGCTTGAATCAACCCAG-GAGAGT 727
 QY 226 AlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlnLeuProlyg 243
 DB 728 GCTTCTACTGATGATGAAATCAGTCTCCCGATCATCATGAAGAACTGCCAAA 781
 RESULT 43
 BE896915 688 bp mRNA linear EST 20-OCT-2000
 LOCUS 60139437F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924560 5',
 DEFINITION mRNA sequence.
 ACCESSION BE896915
 VERSION BE896915.1 GI:10361827
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 688)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTP/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM9762 row: 1 column: 09
 High quality sequence stop: 685.
 Location/Qualifiers

FEATURES

source

1. 688
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3924560"
 /issue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 72"
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 5,396-79 Length: 688
 Score: 934.00 Matches: 185
 Percent Similarity: 97.88% Conservative: 0
 Best Local Similarity: 97.88% Mismatches: 3
 Query Match: 71.79% Indels: 3
 DB: 2 Gaps: 0

US-10-063-734-122 (1-243) x BE896915 (1-688)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 DB 117 ATGGACCCCAAGGCGCCGCGCTCCCGACGCGGCTCCGCGCTCTGCTGCTCTG 176
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnysAla 40
 DB 177 CTGCTGACAGTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGGAGCG 236
 QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyrAnsglyMetCysLeuGlnGlyProAla 60
 DB 237 CAGCTCCGCAAGGAGAGGTGAGCTGTATATGCAATGCTTACACAGGCGACGA 296
 QY 61 GlyAlaProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 DB 297 GGAAGTCCGTGTCGAGAGCGAGCCCTGGGCAATGCAATCCGCGTCACTCGGATC 356
 QY 81 ProGlyArgAspGlyPheLysGlyGlyGlyCysLeuArgGlySerPheGlyGln 100
 DB 357 CCAGGTCCGAGATGATTCAAAGAGAAAAGGGGGAATGCTGAGGAAAGCTTTGAGGAG 416
 QY 101 SerTPThrProAnThrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 417 TCTGGACACCCCACTACAGAGAGTTCATGAGTTCATTAAATTAAGCATAGATCTT 476
 QY 121 GlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 477 GGAATAATTCGAGAGTATCATTTACAAAGAGCGCTTCAATATGCTCTAAGAGT-TTG 535
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrpThr 160
 DB 536 TTCAGTGGCTCACTTCGCTAAATGCAAGAAATGATGCTGCAAGC-TGGTATTTTCA 594
 QY 161 PheAnsglyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180

sequence.
Plate: 0050 row: h column: 6
Seq primer: M13R.
Location/Qualifiers
source

1..790
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/db_xref="taxon:8022"
/clone="tcdbk0050c.h.06"
/issue_type="multi-issues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="cdk"
/note="Vector: pTT73D-pac; AGENAE Rainbow trout
multi-issues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre, Francois PIUMI,
Francois Plumiojouy, Inra, Ir, INRA, CEA Radiobiologie et
Etude du genome (URBG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Alignment Scores:
Pred. No.: 2,466-77 Length: 720
Score: 917.50 Matches: 166
Percent Similarity: 89.32% Conservative: 18
Best Local Similarity: 80.58% Mismatches: 21
Query Match: 70.52% Indels: 1
DB: 5 Gaps: 1
US-10-063-734-122 (1-243) x BX84616 (1-790)

QY 38 GlnlyValaGlnleuArgGlnArgGlnValaValaPleuTyrAsnGlyMetCysleuGln 57
Db 1 AAAAAAGGCACTTGACAGAGAGATGTTGAATACGAAAGTACAAACGCG---TGCCCCCG 57
QY 58 GlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThr 77
Db 58 GGTCCGCGCTGACCCCTGGAAGAGGTAACCTCGGACCAATGGACTCCCTGGACT 117
QY 78 ProGlyIleProGlyArgAspGlyPheGlyGlyValGlyCysleuArgGlnSer 97
Db 118 CCGGACATCCCGGGGCGCATGCAAGGGGAGAAAGAGAGTGTGTAGTGAGTG 177
QY 98 PheGlnGlnSerTyrThrProAsnTyrGlnCysSerTyrSerSerIleuAsnTyrGly 117
Db 178 TTGAGAGACCATGAAACCACTACAGAGTGTGAGTGAAGACCGCTGCGCAGGCTTG 237
QY 118 IleAspLeuGlyIleValaGlnCysThrPheThrIleMetArgSerAsnSerIleu 137
Db 238 ATGACCTGGGCAAAATGACTGACTTACATTCACCAAGCTGCTTCAAGAGTCCCTG 297
QY 138 ArgValIleuPheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyr 157
Db 298 CGTGTGCTCTTCAGGCGCTCCCTGAGGCTGAAGTGAAGACCGCTGCGCAGGCTTG 357
QY 158 TyrPheThrPheAsnGlyValaGlnCysSerGlyProleuProIleGlnAlaIleIleTyr 177
Db 358 TACTTCACCTTCACAGAGCTGAGTGTACAGAGCTCTCCCATTCGAATTCATCTAC 417
QY 178 LeuAspGlnGlySerProGlyMetAsnSerThrIleAsnIleHisArgThrSerSerVal 197
Db 418 CTCGACCAAGGAGCCCTGAGCTCACTCAACCATTAACATACACAGAACCTCATCTGTT 477
QY 198 GlnGlyLeuGlyGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPValGlyThr 217
Db 478 GAAGGCTGTGTGAGGAGATCCGGGAGGCGCTGTGAGCTATCTGGGTGGGAGCA 537
QY 218 CysSerAspTyrProIleGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIle 237
Db 538 TGTGCTGACTACCCAGAGAGAGCGCATCTACAGGCTGAACTGTATCCAGGGTCTTC 597
QY 238 IleGlnGlnleuProlys 243

Db 598 ATAGAGAGCTGCCCAA 615

RESULT 46
CN394775 571 bp mRNA linear EST 16-MAY-2004
LOCUS 17000532586464 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN394775
ACCESSION CN394775
VERSION CN394775.1 GI:47382370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 571)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 571 Std Error: 0.00.
Location/Qualifiers
1..571
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/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/note="Oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 1,776-77 Length: 571
Score: 917.00 Matches: 170
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 70.48% Indels: 0
DB: 7 Gaps: 0
US-10-063-734-122 (1-243) x CN394775 (1-571)

QY 1 MetArgProGlnGlyProAlaIleAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 57 ATGCAACCCAGAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCTGCTCTCCG 116
QY 21 LeuLeuGlnLeuProAlaIleProSerSerAlaSerGlnIleProGlyGlyValGly 40
Db 117 CTGCTGAGCTGCGCGCGCGCTGAGCTGATCCCAAGGAGGAGGAGGAGGAGG 176
QY 41 GlnLeuArgGlnArgGlnValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 177 CAGCTCCGCGAGAGAGAGTGTGACCTGTATATGAAATGTCTTACAAAGGCGCAGCA 236
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 237 GGAAGTGCCTGCTGCGAGAGGAGGAGCCCTGGGCGCAATGGCATTCGGGTATCCTG 296
QY 81 ProGlyArgAspGlyPheGlyGlyValGlyGlyGlyCysLeuArgGlnSerPheGlnGln 100
Db 297 CCAGTCCGAGATGATTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356

QY 101 SerTTPTh-ProAsnTyrIysGlnCysSerTSPSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 357 TCTTGAGACACCACTACAGAGCAGTGTTCATGAGTTCATTAATGACATAGATCTT 416
 QY 121 GtLVsIIAlAGlucYsthrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 417 GGGAAATATGGAGAGTACATTAACAAGATCGTTCAAAATAGTCTCTAAGAGTTTGG 476
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 DB 477 TTCAGTGGCTCACTTCGGCTAAATGCAAGAAATGCAATGCTGTCAGCGTTGGATTTCACA 536
 QY 161 PheAnGlyAlAGlucYsSerGlyProLeuPro 171
 DB 537 TTCATGAGAGCTGAATGTCAGAGCTCTTCCC 569
 RESULT 47
 LOCUS BX299779 641 bp mRNA linear EST 10-MAY-2004
 DEFINITION BX299779 tcay Oncorhynchus mykiss cdna clone tcay0005b.n.07 5prim,
 mRNA sequence.
 ACCESSION BX299779
 VERSION BX299779.2 GI:42613305
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Proclanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 641)
 Govoroun M., Guiguen Y. and Le Gac F.
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, *Oncorhynchus mykiss*
 Unpublished (2003)
 On Apr 7, 2003 this sequence version replaced GI:29580424.
 CONTACT: Guiguen Y
 INRA - SCRIBE
 Campus de beaulieu, RENNES cedex, 35042, France
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 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigena@portel.jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0005 row: n column: 7
 Seq primer: M13R.
 FEATURES
 SOURCE
 1.641
 Location/Qualifiers
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 differentiating gonads, gills, intestinal, intestine,
 kidney, liver, muscle, ovary, pituitary, testis"
 /dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /clone_lib="tcay"
 /note="vector: pT7T3D-pac; Rainbow trout multi-tissues -
 normalized + 1 subtraction (tcay) ; Clone distribution :
 AGENAE Resource centre. Francois PUDM,
 Francois.Piumi@jouy.inra.fr, INRA, CRA Radiobiologie et
 Etude du genome (LREG), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.09e-76 Length: 641
 Score: 906.50 Matches: 165
 Percent Similarity: 88.35% Conservative: 17
 Best Local Similarity: 80.10% Mismatches: 23
 Query Match: 69.68% Indels: 1

DB: 5 Gaps: 1
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 QY 58 GlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThr 77
 DB 59 GGTTCGGCTGACCCCTCGAAGGAGAGGTAACTCTGGACCAATGGCATCCCTGGAGACT 118
 QY 78 ProGlyIleProGlyArgAspGlyPheIysGlyValIysGlyGluCysLeuArgGlySer 97
 DB 119 CTTGACATCCCGGGGCGGATGCGATCAAGGGGAGAAAGAGAGTGTGAGTGAAGGTG 178
 QY 98 PheGluIysSerTyrThrProAsnTyrIysGlnCysSerTSPSerSerLeuAsnTyrGly 117
 DB 179 TTTGAGGAGCATGAGAAACCACTACAGACAGTGTCTGGAATCATTGAGTGG 238
 QY 118 IleAspLeuGlyValIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeu 137
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 QY 138 ArgValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyr 157
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 QY 158 TyrPheThrPheAnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyr 177
 DB 359 TACTTCACCTTTCACGAGAGCTGAGTGAACGAGACCTTGGCCATTCATCATCTAC 418
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 QY 218 CysSerAspTyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIle 237
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 VERSION BQ424201.1 GI:21119516
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 1 (bases 1 to 902)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCID/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>

